STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 167420

TO: Lorraine Spector **Location: 4d55 / 4c70** **Monday, October 03, 2005** **Art Unit: 1647** **Phone: 571-272-0893** **Serial Number: 09 / 674377**	**From: Jan Delaval** **Location: Biotech-Chem Library** **Remsen 1a51** **Phone: 571-272-2504** **jan.delaval@uspto.gov**

Search Notes

Rest 10/4/05

167420

STIC-Biotech/ChemLib

From: Spector, Lorraine
Sent: Friday, September 30, 2005 1:42 PM
To: STIC-Biotech/ChemLib
Subject: SEARCH request for Serial No. 09/674377

STIC,

Please search SEQ ID NO: 1 and 2
-pending
-issued
-commercial
Also, please align the two sequences with each other.
Thanks.

Lorraine Spector
571-272-0893
U.S. Patent and Trademark Office
Art Unit 1647
lorraine.spector@uspto.gov
Office: Remsen 4D-55
Mailbox: Remsen 4C-70

****
Searcher: Jan
Searcher Phone: 22504
Date Searcher Picked up: 10/3/05
Date completed: 10/3/05
Searcher Prep Time: 10
Online Time: 20

****
Type of Search
NA#_____ AA#: 1
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM: ✓
WWW/Internet:_____
Other (Specify):_____

STIC SEARCH RESULTS FEEDBACK FORM

USPTO

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact***:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

  Types of relevant prior art found:
  - ☐ Foreign Patent(s)
  - ☐ Non-Patent Literature
    (journal articles, conference proceedings, new product announcements etc.)
- *Relevant prior art **not found**:*
  - ☐ Results verified the lack of relevant prior art (helped determine patentability).
  - ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.

sira
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 40.225 Seconds
(without alignments)
1069.209 Million cell updates/sec

Title: US-09-674-377B-1
Perfect score: 2604
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2601	99.9	728	1	JH0579	hepatocyte growth
2	2408	92.5	728	1	A60185	hepatocyte growth
3	2401	92.2	728	1	A35644	hepatocyte growth
4	1864.5	71.6	710	1	I51283	hepatocyte growth
5	1737.5	66.7	411	2	I51285	hepatocyte growth
6	1180.5	45.3	711	1	A47136	macrophage-stimula
7	1144	43.9	716	1	JC5061	macrophage-stimula
8	1125	43.2	716	1	A40332	macrophage-stimula
9	1066	40.9	790	1	PLPG	plasmin (EC 3.4.21
10	1059	40.7	812	1	PLMS	plasmin (EC 3.4.21
11	1053.5	40.5	810	2	I46260	plasmin (EC 3.4.21
12	1044.5	40.1	810	2	B30848	plasmin (EC 3.4.21
13	1042	40.0	810	1	PLHU	plasmin (EC 3.4.21
14	1038	39.9	812	1	PLBO	plasmin (EC 3.4.21
15	943.5	36.2	2869	2	T18518	apolipoprotein(a)
16	879	33.8	4548	1	S00657	apoprotein(a) (EC
17	843.5	32.4	1420	2	A32869	apolipoprotein(a)
18	457	17.5	460	2	B61545	plasmin (EC 3.4.21
19	454	17.4	455	2	A61545	plasmin (EC 3.4.21
20	408.5	15.7	336	2	S33879	plasmin precursor
21	357.5	13.7	625	1	TBBO	thrombin (EC 3.4.2
22	353	13.6	169	2	A40522	plasmin (EC 3.4.21
23	352.5	13.5	618	2	A35827	thrombin (EC 3.4.2
24	350	13.4	622	1	TBHU	thrombin (EC 3.4.2
25	344	13.2	617	2	S10511	thrombin (EC 3.4.2
26	307.5	11.8	559	1	A35029	t-plasminogen acti
27	303	11.6	562	1	UKHUT	t-plasminogen acti
28	297.5	11.4	559	1	A29941	t-plasminogen acti
29	270	10.4	120	2	E61545	plasmin (EC 3.4.21
30	268	10.3	123	2	C61545	plasmin (EC 3.4.21
31	260.5	10.0	89	2	A60140	plasmin (EC 3.4.21
32	235.5	9.0	946	1	A47299	ror-related recept
33	230	8.8	943	2	B45082	neurotrophic recep
34	228.5	8.8	603	2	S28941	coagulation factor
35	225.5	8.7	291	2	I38098	t-plasminogen acti
36	217	8.3	937	2	A45082	neurotrophic recep
37	204	7.8	655	1	A46688	hepatocyte growth
38	195	7.5	615	1	KFHU12	coagulation factor
39	192.5	7.4	558	2	JC5878	plasma hyaluronan-
40	189	7.3	593	2	S45281	coagulation factor
41	186.5	7.2	560	1	JC4795	plasma hyaluronan-
42	182	7.0	806	2	T18840	hypothetical prote
43	159	6.1	685	1	A48289	neurotrophic recep
44	158.5	6.1	433	1	JN0560	u-plasminogen acti
45	158	6.1	442	1	UKPG	u-plasminogen acti

ALIGNMENTS

RESULT 1
JH0579
hepatocyte growth factor precursor [validated] - human
N;Alternate names: hepapoietin A; scatter factor
C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S06
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Title: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Accession: JH0579
A;Molecule type: DNA
A;Residues: 1-728 <SEK>
A;Cross-references: UNIPROT:P14210; DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333
A;Accession: JU0333
A;Molecule type: DNA
A;Residues: 1-481,'RT',484-728 <SE2>
R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth f
A;Reference number: A41140; MUID:91334393; PMID:1831266
A;Accession: A41140
A;Molecule type: mRNA
A;Residues: 1-728 <WEI>
A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth facto
A;Reference number: A36677; MUID:91025062; PMID:2145836
A;Accession: B36677
A;Molecule type: mRNA
A;Residues: 1-728 <SE3>
A;Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032
A;Accession: A36677
A;Molecule type: mRNA
A;Residues: 1-161,167-728 <SE4>
A;Cross-references: EMBL:X16323
A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A;Reference number: A33512; MUID:89392017; PMID:2528952
A;Accession: A33512
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-728 <MIY>

A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A;Reference number: A39006; MUID:91110540; PMID:1824873
A;Accession: A39006
A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M55379
A;Experimental source: embryonic lung
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native and
A;Reference number: PH0114; MUID:91207365; PMID:1826837
A;Accession: PH0114
A;Molecule type: protein
A;Residues: 32-43;53-58 <YOS>
A;Experimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Accession: A37796
A;Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',5
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashi
Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676; PMID:2531289
A;Accession: S06794
A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,'
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
A;Experimental source: liver
A;Note: the authors translated the codon CAG for residue 727 as Glu
A;Note: part of this sequence, including the amino end of both the alpha and beta chains
R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
A;Reference number: I59214; MUID:93087571; PMID:1280830
A;Accession: I59214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-288,'ET' <HAR>
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor g
A;Reference number: S15443; MUID:91200041; PMID:1826653
A;Accession: S15443
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-288,'ET' <MIY2>
A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
A;Reference number: I52253; MUID:92062058; PMID:1835383
A;Accession: I52253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 161-166 <SHI>
A;Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
C;Genetics:
A;Gene: GDB:HGF
A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homold
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F;32-494/Domain: alpha chain #status experimental <ACH>
F;128-206/Domain: kringle homology <KR1>
F;211-288/Domain: kringle homology <KR2>
F;305-383/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR4>
F;495-728/Domain: beta chain #status experimental <BCH>
F;495-716/Domain: trypsin homology <TRY>
F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;487-604/Disulfide bonds: #status predicted

Query Match 99.9%; Score 2601; DB 1; Length 728;
Best Local Similarity 99.8%; Pred. No. 1.9e-176;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 2
A60185
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; JU0231
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep
A;Reference number: JC2117; MUID:94183257; PMID:8135822
A;Accession: JC2117
A;Molecule type: mRNA
A;Residues: 1-728 <SAS2>
A;Cross-references: UNIPROT:Q08048; GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436
A;Experimental source: fibroblast, COS-1 cell
A;Note: submitted to JIPID, May 1993
A;Accession: PC2064
A;Molecule type: protein
A;Residues: 496-504 <SA2>
R;Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

A;Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig
A;Reference number: A60185; MUID:90377927; PMID:2144630
A;Accession: A60185
A;Molecule type: protein
A;Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,'
R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A;Reference number: S43416; MUID:94060105; PMID:8241272
A;Accession: S43416
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <LIU>
A;Cross-references: EMBL:X72307
R;Liu, Y.
submitted to the EMBL Data Library, May 1993
A;Reference number: S45521
A;Accession: S45521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563,'H',565-728 <LI2>
A;Cross-references: EMBL:X72307
R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A;Title: Purification and characterization of biologically active scatter factor from ra
A;Reference number: S17173; MUID:91354223; PMID:1831975
A;Accession: S17173
A;Molecule type: protein
A;Residues: 496-517,'T',519 <COF>
R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A;Title: Hepatocytes and scatter factor.
A;Reference number: S10966; MUID:90326152; PMID:2142751
A;Accession: S10966
A;Status: preliminary
A;Molecule type: protein
A;Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Reference number: I48758; MUID:95122532; PMID:7822318
A;Accession: I48758
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-30 <RES>
A;Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495,496-728/Product: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

Query Match 92.5%; Score 2408; DB 1; Length 728;
Best Local Similarity 91.1%; Pred. No. 8.6e-163;
Matches 407; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| |||||||||||||||||||| |||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | |||||||||| : :|:||||:|||||||||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:|||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||:|||||||||||||||||||||||||||||:||||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479
```

RESULT 3
A35644
hepatocyte growth factor precursor - rat
N;Alternate names: hepapoietin A; scatter factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
C;Accession: A35644; S13211
R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamur
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of the
A;Reference number: A35644; MUID:90222197; PMID:2139229
A;Accession: A35644
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <TAS>
A;Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133.1;
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
R;Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur
A;Reference number: S13211; MUID:91031482; PMID:2146117
A;Accession: S13211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495/Product: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

```
  Query Match             92.2%;  Score 2401;  DB 1;  Length 728;
  Best Local Similarity   90.4%;  Pred. No. 2.7e-162;
  Matches  404;  Conservative   23;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||| | || :||||||||:||:||||| |||| ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLVKIKTKKVNSADECANRCIRNKGFPFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:||||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | ||||||| || : :|:||||:||||||:||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKMCAHSAVNETDVPMETTECIKGQGEGYRGTTNTIWNGIPCQRWDS 332

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:|||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              |||||||||||||:|||||||||||||||||||||||||||| :|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLTKNYCRNPDDDAHGPW 452

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||:||||||||||||||||||
Db        453 CYTGNPLVPWDYCPISRCEGDTTPTIV 479


RESULT 4
I51283
hepatocyte growth factor precursor - clawed frog
N;Alternate names: hepapoietin A; scatter factor
C;Species: Xenopus sp. (clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-May-2004
C;Accession: I51283
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Mech. Dev. 49, 123-131, 1995
A;Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
A;Reference number: I51283; MUID:95267690; PMID:7748783
A;Accession: I51283
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-710 <NAK>
A;Cross-references: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933
A;Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F;42-477,478-709/Product: hepatocyte growth factor #status predicted <MAT>
F;42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;115-193/Domain: kringle homology <KR1>
F;198-275/Domain: kringle homology <KR2>
F;289-367/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR4>
F;478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;478-700/Domain: trypsin homology <TRY>
F;52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
F;470-588/Disulfide bonds: #status predicted

  Query Match             71.6%;  Score 1864.5;  DB 1;  Length 710;
  Best Local Similarity   69.3%;  Pred. No. 2.3e-124;
  Matches  305;  Conservative   64;  Mismatches   68;  Indels    3;  Gaps    1;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |:||   ::||:|:||| ::: ||::|||  || : || ||:|||||||||||| |||
Db         21 KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI 80

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| || ||:||:|:| ::   ||||| |||||:|| ||| :|:|| ::|| |: ||||:
Db         81 KRCHWFSFNTMSAGIKDKYDISFDLYEKKDYIRDCIHGKGSNYRGTRNVTKRGLACQPWN 140

Qy        123 SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 182
              |||||||||||:||||||:|||||||:|||||||||| :||||::||||| ||||:|:|
Db        141 SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT 200

Qy        183 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 242
              |||| ||| ||:||||| ||||| | ||:||| |||||:|| :|||||||||: ||||||
Db        201 CNGEHYRGPMDYTESGKECQRWDLQRPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT 260

Qy        243 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 302
              ||| | ||:|||| |  : :|:||:   | :|::|||||||:|:|  :||| |||||||:
Db        261 LDPDTSWEFCAIKPCVHSIVNNTDI---TKDCMKGQGEGYRGSVSTTYNGIQCQRWDSQF 317

Qy        303 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 362
              || |: ||||:||||| ||||||||||||||||||||:|:|||| |  |: |:||
Db        318 PHLHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY 377

Qy        363 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY 422
              |||  | | ||:||  | ||||:||::|| || | ||| | | :|||||||:||||||||
Db        378 GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY 437

Qy        423 TGNPLIPWDYCPISRCEGDT 442
              | :| :|||||||||||||
Db        438 TDDPFVPWDYCPISRCEGDT 457


RESULT 5
I51285
hepatocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51285
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
A;Reference number: I51285; MUID:95237013; PMID:7720585
A;Accession: I51285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-411 <STR>
A;Cross-references: UNIPROT:Q90978; GB:S77480; NID:g998675; PID:g998676
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
F;124-197/Domain: kringle homology <KRG>
F;202-279/Domain: kringle homology <KR2>
F;296-374/Domain: kringle homology <KR3>

  Query Match             66.7%;  Score 1737.5;  DB 2;  Length 411;
  Best Local Similarity   74.9%;  Pred. No. 1.3e-115;
  Matches  289;  Conservative   47;  Mismatches   45;  Indels    5;  Gaps    1;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:||||| |||||| :|:
Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:||||||||  ||||:|||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 182
              |||||||     |||||||:|||||||||||||||::|:|:|||||| ||||||||
Db        150 SMIPHEH-----SYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMT 204

Qy        183 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 242
```

```
                ||||||||| |||||||| ||||| | ||:||| ||||||||||||||||||: ||||||
Db        205 CNGESYRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYT 264

Qy        243 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 302
                ||||| ||:|||||    :| |:   ||| ||||||||||||||||:|| |||||||:
Db        265 LDPNTPWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQF 324

Qy        303 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 362
                ||:|::|||||||||||||||||||||||||||||||||:||||||| ||:|: |||||
Db        325 PHQHNITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYR 384

Qy        363 GNGKNYMGNLSQTRSGLTCSMWDKNM 388
                ||||:|||||||:|| ||||| |||||
Db        385 GNGKSYMGNLSKTRFGLTCSTWDKNM 410


RESULT 6
A47136
macrophage-stimulating protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
C;Accession: A40331; B40331; A47136; A61395
R;Han, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A;Title: Characterization of the DNF15S2 locus on human chromosome 3: identification of
A;Reference number: A40331; MUID:92002016; PMID:1655021
A;Accession: A40331
A;Molecule type: DNA
A;Residues: 1-711 <HA1>
A;Cross-references: UNIPROT:P26927; GB:M74179
A;Accession: B40331
A;Molecule type: mRNA
A;Residues: 1-711 <HA2>
A;Cross-references: GB:M74178; NID:g183976; PIDN:AAA50165.1; PID:g183977
R;Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A;Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MS
A;Reference number: A47136; MUID:93340141; PMID:8393443
A;Accession: A47136
A;Molecule type: mRNA
A;Residues: 1-12,'C',14-622,'F',624-711 <YOS>
A;Cross-references: GB:L11924; NID:g398037; PIDN:AAA59872.1; PID:g398038
A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence
R;Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
J. Exp. Med. 173, 1227-1234, 1991
A;Title: Macrophage stimulating protein: purification, partial amino acid sequence, and
A;Reference number: A61395; MUID:91217635; PMID:1827141
A;Accession: A61395
A;Molecule type: protein
A;Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Experimental source: plasma
C;Genetics:
A;Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
A;Cross-references: GDB:128833; OMIM:142408
A;Map position: 3p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;19-483/Domain: alpha chain #status predicted <ACH>
F;110-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR3>
F;370-448/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status predicted <BCH>
F;484-704/Domain: trypsin homology <TRY>
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           45.3%;  Score 1180.5;  DB 1;  Length 711;
  Best Local Similarity  47.4%;  Pred. No. 5.6e-76;
  Matches  197;  Conservative   62;  Mismatches  148;  Indels    9;  Gaps    4;

Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
                |  |::|| ||    |    |:|| :: :   |   |:   |   :       ||:: ||
Db         50 VADAEECAGRC----GPLMDCRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 152
               |:| ||:  |  |:|||:: |  |: || ||   |::| : |:   |  |:||:|||| |:
Db        106 YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEENFCRNPDGD 163

Qy        153 EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 212
                |||||:|::| ||:: | |  | |  |: |||| ||| :| |||| | ||:|
Db        164 PGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQH 223

Qy        213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETT 272
                | | :: |:| ||||||||||  |||||| ||    |:| :  |        :   |
Db        224 PFEPGKFLDQGLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTV 281

Qy        273 ECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESP 332
                | :|:|||||||  ||   |:||||||:| ||:|  ||| : |||||||:||||||||:|
Db        282 SCFRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAP 341

Qy        333 WCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDL 391
                ||||  | :|  :| ||  | |    |||| | |: | | :|:|| |: |  |
Db        342 WCFTLRPGMRAAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQCQRWSAETPHK 401

Qy        392 HRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV 447
                :  |     ::| ||:||||| |:|||||| :|  |:||| : ||  |  |:|:
Db        402 PQFTFTSEPHAQLEENFCRNPDGDSHGPWCYTMDPRTPFDYCALRRCADDQPPSIL 457


RESULT 7
JC5061
macrophage-stimulating protein 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5061
R;Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, N
Biochem. Biophys. Res. Commun. 227, 273-280, 1996
A;Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in
A;Reference number: JC5061; MUID:97011126; PMID:8858136
A;Accession: JC5061
A;Molecule type: mRNA
A;Residues: 1-716 <OHS>
A;Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g16
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
F;110-186/Domain: kringle homology <KRI1>
F;191-268/Domain: kringle homology <KRI2>
F;292-370/Domain: kringle homology <KRI3>
F;379-457/Domain: kringle homology <KRI4>
F;489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match           43.9%;  Score 1144;  DB 1;  Length 716;
  Best Local Similarity  46.1%;  Pred. No. 2.1e-73;
  Matches  196;  Conservative   70;  Mismatches  141;  Indels   18;  Gaps    6;

Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
                |  |::|| ||    |    |:|| :: :   |   |:   |   :       ||:: ||
Db         50 VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLRAQLHHSSLCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 152
               |:| ||:  | ||:|||: |  |: || ||   |::| : |:   |  |:||:|||| |:
Db        106 YVRTCIMDNGASYRGTVARTADGLPCQAWSRRFPNDHKYTPTPKNG--LEENFCRNPDGD 163

Qy        153 EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 212
                ||||:|:|  ||:: | |  | |  |: |||| ||| :| |||| ||||| | || |
Db        164 PRGPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSH 223
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Qy        213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-------TMNDT 265
Db        224 PFHPEKFPDKALKDNYCRNPDASERPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQQ 283

Qy        266 DVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRN 325
Db        284 RNKVKASNCFRGKGEDYRGTTNTTSAGVPCQRWDAQNPHQHRFVPEKYACKDLRENFCRN 343

Qy        326 PDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMW 384
Db        344 PDGSEAPWCFTSRPGLRVAFCYQIPRCTEEVVPEGCYHGSGEQYRGSVSKTRKGVQCQHW 403

Qy        385 DKNMEDLHRHIFWEPDA--SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 442
Db        404 --SSETPHKPQFTPTSAPHAGLEANFCRNPDGDSHGPWCYTLDPETLFDYCALKRCDDDQ 461

Qy        443 TPTIV 447
Db        462 PPSIL 466
```

RESULT 8
A40332
macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatocyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A40332; B40332
R;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
A;Reference number: A40332; MUID:92002017; PMID:1832957
A;Accession: A40332
A;Molecule type: DNA
A;Residues: 1-716 <DEG>
A;Cross-references: UNIPROT:P26928; GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
A;Accession: B40332
A;Molecule type: mRNA
A;Residues: 1-18,'P',20-716 <DEG2>
A;Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C;Genetics:
A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F;19-483/Domain: alpha chain #status experimental <ACH>
F;110-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;292-370/Domain: kringle homology <KR3>
F;379-457/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status experimental <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 43.2%; Score 1125; DB 1; Length 716;
  Best Local Similarity 45.9%; Pred. No. 4.7e-72;
  Matches 195; Conservative 69; Mismatches 143; Indels 18; Gaps 6;

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Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
Db         50 VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLHTQLYHSSLCHLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 152
Db        106 YVRTCIMDNGVSYRGTVARTAGGLPCQAWSRRFPNDHKYTPTPKNG--LEENFCRNPDGD 163

Qy        153 EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 212
Db        164 PRGPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSH 223
```

```
Qy        213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-------TMNDT 265
Db        224 PFQPEKFLDKDLKDNYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQR 283

Qy        266 DVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRN 325
Db        284 RNKGKALNCFRGKGEDYRGTTNTTSAGVPCQRWDAQSPHQHRFVPEKYACKDLRENFCRN 343

Qy        326 PDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMW 384
Db        344 PDGSEAPWCFTSRPGLRMAFCHQIPRCTEELVPEGCYHGSGEQYRGSVSKTRKGVQCQHW 403

Qy        385 DKNMEDLHRHIFWEPDASK--LNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDT 442
Db        404 --SSETPHKPQFTPTSAPQAGLEANFCRNPDGDSHGPWCYTLDPDILFDYCALQRCDDDQ 461

Qy        443 TPTIV 447
Db        462 PPSIL 466
```

RESULT 9
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A;Reference number: S03733
A;Accession: S03733
A;Molecule type: protein
A;Residues: 1-560 <SCH>
A;Cross-references: UNIPROT:P06867
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
A;Molecule type: protein
A;Residues: 1-57 <BRU>
R;Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F;1-790/Product: plasminogen #status predicted <PRO>
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 40.9%; Score 1066; DB 1; Length 790;
Best Local Similarity 44.6%; Pred. No. 7.8e-68;
Matches 195; Conservative 65; Mismatches 137; Indels 40; Gaps 13;

```
Qy         25 ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 84
              :|  |     : ::|| :|       | |:|| :    :||:    || :| : :    :
Db         16 SLSRKQVAARSVEECAAKCEAETN--FICRAFQYHSKDQQCVVMAENSKTSPIARM--RD 71

Qy         85 FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQEN 144
                |:| : |:  |  | |::|:||| | ||||: || ||   ||   : |  :    |:||
Db         72 VVLFEKRIYLSECKTGNGKNYRGTTSKTKSGVICQKWSVSSPHIPKYSPEKFPLAGLEEN 131

Qy        145 YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 204
              |||||  :| ||||:|::|| |:: ||||:| | ||| |:|| | | :  | ||  || |
Db        132 YCRNPDNDEKGPWCYTTDPETRFDYCDIPEC-EDECMHCSGEHYEGKISKTMSGIECQSW 190

Qy        205 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMND 264
                |:|| | :|| ::|:|    ||||||||:|||||:| ||: |||:| |  |   |
Db        191 GSQSPHAHGYLPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPNKRWEFCDIPRC--TTPPP 248

Qy        265 TDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 324
              |  |  | :|::|:|| |||||:   :|  |||| :| ||:|: ||||| ||:| |||||
Db        249 TSGP--TYQCLKGRGENYRGTVSVTASGHTCQRWSAQSPHKHNRTPENFPCKNLEENYCR 306

Qy        325 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMS-----H------------GQDCYRGNGKN 367
              ||||  :|||:|||  :|  || :||:|  |      |                ||||||::
Db        307 NPDGETAPWCYTTDSEVRWDYC-KIPSCGSSTTSTEHLDAPVPPEQTPVAQDCYRGNGES 365

Qy        368 YMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE------PDASKLNENYCRNPDDDAHGPWC 421
              | |  | | :|  | |       |||   |      |:|  |  |||||| |   |||
Db        366 YRGTSSTTITGRKCQSWVSMTP--HRH---EKTPGNFPNAG-LTMNYCRNPDAD-KSPWC 418

Qy        422 YTGNPLIPWDYCPISRC 438
              || :| : |:|| : :|
Db        419 YTTDPRVRWEYCNLKKC 435
```

RESULT 10
PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of t
A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514
A;Molecule type: mRNA
A;Residues: 1-812 <DEG>
A;Cross-references: UNIPROT:P20918; GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LI2>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin
mediately after dissociation from the clot. In the presence of the inhibitor, the activa
e inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. To
eful in treating solid tumors.
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-812/Product: plasminogen #status predicted <PRO>
F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <MAT>
F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
bonds: #status predicted
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

Query Match 40.7%; Score 1059; DB 1; Length 812;
Best Local Similarity 43.3%; Pred. No. 2.5e-67;
Matches 191; Conservative 67; Mismatches 145; Indels 38; Gaps 12;

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Qy         30 TKKVNTA---DQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||   |     |  :|       | |::| :    :||:    || :| : :    :
Db         37 TKKQLAAGGVSDCLAKCEGE--TDFVCRSFQYHSKEQQCVIMAENSKTSSIIRM--RDVI 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYC 146
              |:|  : |:  |  | |  |:||:| ||||: || | :  ||  :: ||::  : |:||||
Db         93 LFEKRVYLSECKTGIGNGYRGTMSRTKSGVACQKWGATFPHVPNYSPSTHPNEGLEENYC 152

Qy        147 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 206
              |||  :| ||||:|::|: ||: |:||:| | ||| |:|| | | :  | ||  || ||
Db        153 RNPDNDEQGPWCYTTDPDKRYDYCNIPECEE-ECMYCSGEKYEGKISKTMSGLDCQAWDS 211

Qy        207 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 266
              |:|| | ::| ::| |    ||| ||||:|||||:| ||  |||||  |  |
Db        212 QSPHAHGYIPAKFPSKNLKMNYCHNPDGEPRPWCFTTDPTKRWEYCDIPRCT----TPPP 267

Qy        267 VPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNP 326
              |  | :|::|:|| |||||:   :|  ||||  | || |: |||||  ||:| |||||||
Db        268 PPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNP 327

Qy        327 DGSESPWCFTTDPNIRVGYCSQIPNCDMSHG-----------------QDCYRGNGKNYM 369
              ||  :|||:|||  :|  || :||:|: |                   |:||: :|::|
Db        328 DGETAPWCYTTDSQLRWEYC-EIPSCESSASPDQSDSSVPPEEQTPVVQECYQSDGQSYR 386

Qy        370 GNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNP 426
              |  | | :|  |  |       |||       |||  |  ||||||| |  |||||| :|
Db        387 GTSSTTITGKKCQSWAAMFP--HRHSKTPENFPDAG-LEMNYCRNPDGD-KGPWCYTTDP 442

Qy        427 LIPWDYCPISRCEGDTTPTIV 447
              : |:|| : ||  :|  ::|
Db        443 SVRWEYCNLKRC-SETGGSVV 462
```

RESULT 11
I46260
plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46260
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fon
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipopro
A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: I46260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

```
A;Residues: 1-810 <LAW>
A;Cross-references: UNIPROT:Q29485; EMBL:U33171; NID:g1046360; PID:g1046361
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;379-456/Domain: kringle homology <KR4>
F;482-561/Domain: kringle homology <KR5>
F;582-803/Domain: trypsin homology <TRY>

  Query Match             40.5%;  Score 1053.5;  DB 2;  Length 810;
  Best Local Similarity   44.3%;  Pred. No. 6.1e-67;
  Matches  194;  Conservative   63;  Mismatches  138;  Indels   43;  Gaps   13;

Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||    | : ::|| :|   |   | |::| :    :||:    || |: | :    :
Db         37 TKKQLSVGSTEECAVKC--EKETSFICRSFQYHSKEQQCVIMAENSKSTPVLRM--RDVI 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYC 146
              |:| | |:  | :| |: |:|||| ||:|: || ||:  ||:  | |     : | :|||
Db         93 LFEKKMYLSECKVGNGKYYRGTVSKTKTGLTCQKWSAETPHKPRFSPDENPSEGLDQNYC 152

Qy        147 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 206
              |||  :  ||||:| :|||||| |:| || | ||| |:|::| | :  | ||  || ||
Db        153 RNPDNDPKGPWCYTMDPEVRYEYCEIIQC-EDECMHCSGQNYVGKISRTMSGLECQPWDS 211

Qy        207 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 266
              | || | |:| ::| |    ||||||||:|||||:|:| : ||||| |  |       |
Db        212 QIPHPHGFIPSKFPSKNLKMNYCRNPDGEPRPWCFTMDRNKRWEYCDIPRCT------TP 265

Qy        267 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 324
               |    | :|: | || |:| |    :|: |||  | || || ||||: ||:| |||||
Db        266 PPPSGPTYQCLMGNGEHYQGNVAVTVSGLTCQRWGEQSPHRHDRTPENYPCKNLDENYCR 325

Qy        325 NPDGSESPWCFTTDPNIRVGYCSQIPNC-----DMSHG-------------QDCYRGNG 365
              ||||  :||||||: ::|  :| :||:|     :  |                 |:||:|||
Db        326 NPDGEPAPWCFTTNSSVRWEFC-KIPDCVSSASETEHSDAPVIVPPEQTPVVQECYQGNG 384

Qy        366 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCY 422
              : | |  | | :|  |  |       |||       |||  |  |||||| |  |||||
Db        385 QTYRGTSSTTITGKKCQPWTSMRP--HRHSKTPENYPDAD-LTMNYCRNPDGD-KGPWCY 440

Qy        423 TGNPLIPWDYCPISRCEG 440
              | :| : |::| : :| |
Db        441 TTDPSVRWEFCNLKKCSG 458


RESULT 12
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: B32869
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-810 <TOM>
A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-9/Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted

  Query Match             40.1%;  Score 1044.5;  DB 2;  Length 810;
  Best Local Similarity   42.6%;  Pred. No. 2.6e-66;
  Matches  188;  Conservative   74;  Mismatches  128;  Indels   51;  Gaps   12;

Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||     : ::|| :|   :   |||::| :    :||:    |  || | :    :
Db         37 TKKQLGAGSIEECAAKCEEEE--EFTCRSFQYHSKEQQCVIMAENRKSSIVFRM--RDVV 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYC 146
              |:| | |:  |  | |::|:||:| |::|| || |||  ||  :| |:::  : |:||||
Db         93 LFEKKVYLSECKTGNGKNYRGTMSKTRTGITCQKWSSTSPHRPTFSPATHPSEGLEENYC 152

Qy        147 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 206
              |||  :  ||||:|::||| |:: ||||:| | ||| |:||:| | :  | ||  || ||
Db        153 RNPDNDGQGPWCYTTDPEERFDYCDIPEC-EDECMHCSGENYDGKISKTMSGLECQAWDS 211

Qy        207 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 266
              |:|| | ::| ::|:|    ||||||||:|||||:| ||: ||| | |  |       |
Db        212 QSPHAHGYIPSKFPNKNLKKNYCRNPDGEPRPWCFTTDPNKRWELCDIPRCT------TP 265

Qy        267 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 324
               |    | :|::| || ||| |    :|  |  | :| || |: ||||| ||:| |||||
Db        266 PPSSGPTYQCLKGTGENYRGDVAVTVSGHTCHGWSAQTPHTHNRTPENFPCKNLDENYCR 325

Qy        325 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH-----------------GQDCYRGNGKN 367
              |||| ::|||:||:  :|  || :||:|: |                   |:|| |::
Db        326 NPDGEKAPWCYTTNSQVRWEYC-KIPSCESSPVSTEPLDPTAPPELTPVVQECYHGDGQS 384

Qy        368 YMGNLSQTRSGLTCSMW--------DKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGP 419
              | |  | | :|  |  |       :|  |:      |:|  |  ||||||| |  ||
Db        385 YRGTSSTTTTGKKCQSWSSMTPHWHEKTPENF-------PNAG-LTMNYCRNPDAD-KGP 435

Qy        420 WCYTGNPLIPWDYCPISRCEG 440
              ||:| :| : |:|| : :| |
Db        436 WCFTTDPSVRWEYCNLKKCSG 456


RESULT 13
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A04
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <PET>
A;Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; GB:J05286; GB:M34276
A;Experimental source: leukocyte; lung fibroblast
R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Ta
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in li
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human pl
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
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A;Molecule type: mRNA
A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
R;Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R;Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
A;Molecule type: protein
A;Residues: 581-810 <WI1>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla

A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
A;Molecule type: protein
A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
A;Molecule type: protein
A;Residues: 483-507,'E',509-604 <WI3>
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A;Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A;Reference number: A92125; MUID:73149248; PMID:4694729
A;Contents: annotation; active site
R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A;Reference number: A92382; MUID:82213905; PMID:6919539
A;Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A;Reference number: A92458; MUID:85054794; PMID:6094526
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site

R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.
J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferati
A;Reference number: A58811; MUID:97067211; PMID:8910613
A;Contents: annotation
R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (
A;Reference number: A58812; MUID:9548733; PMID:9548733
A;Contents: annotation
R;Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51488; PDB:2PK4
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A;Reference number: A51911; PDB:1PKR
A;Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R;Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A;Reference number: A52408; PDB:1PMK
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65244; PDB:1CEA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65245; PDB:1CEB
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmi
A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65803; PDB:1HPJ
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65804; PDB:1HPK
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmino
A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a

```
d PIR:FGHUGB).
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af
rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. To
ting solid tumors.
C;Genetics:
A;Gene: GDB:PLG
A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-810/Product: plasminogen #status experimental <PRO>
F;20-96/Domain: activation peptide #status experimental <APT>
F;79-466/Product: angiostatin #status experimental <AST>
F;97-580,581-810/Product: plasmin #status experimental <MAT>
F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>

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  Matches  193;  Conservative   68;  Mismatches  140;  Indels  42;  Gaps   13;

Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||     : ::|| :|  ::   |||:|| :    :||:    |  || : :    :
Db         37 TKKQLGAGSIEECAAKCEEDE--EFTCRAFQYHSKEQQCVIMAENRKSSIIIRM--RDVV 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYC 146
              |:| | |:  |  | |::|:||:| ||:|| || ||| ||   | |::  : |:||||
Db         93 LFEKKVYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYC 152

Qy        147 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 206
              |||  :  ||||:|::|| ||: ||| :| | ||| |:||:| | :  | ||  || ||
Db        153 RNPDNDPQGPWCYTTDPEKRYDYCDILECEE-ECMHCSGENYDGKISKTMSGLECQAWDS 211

Qy        207 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 266
              |:|| | ::| ::|:|    ||||||| : ||||:| ||: ||| | |  |        |
Db        212 QSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCT------TP 265

Qy        267 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 324
               |    | :|::| || ||| |    :|  || | :| || |: ||||| ||:| |||||
Db        266 PPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCR 325

Qy        325 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH----------------GQDCYRGNGKN 367
              ||||  :||| ||:  :|  || :||:|| |                ||||  |:|::
Db        326 NPDGKRAPWCHTTNSQVRWEYC-KIPSCDSSPVSTEQLAPTAPPELTPVVQDCYHGDGQS 384

Qy        368 YMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTG 424
              | |  | | :|  | |      |||       |:|  |  |||||| |  ||||:|
Db        385 YRGTSSTTTTGKKCQSWSSMTP--HRHQKTPENYPNAG-LTMNYCRNPDAD-KGPWCFTT 440

Qy        425 NPLIPWDYCPISRCEGDTTPTIV 447
              :| : |:|| : :| | |  ::|
Db        441 DPSVRWEYCNLKKCSG-TEASVV 462


RESULT 14
PLBO
plasmin (EC 3.4.21.7) precursor - bovine
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: S45046; A25835; I45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BER>
A;Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g4949
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm
A;Reference number: A25835; MUID:85203906; PMID:3846532
A;Accession: A25835
A;Molecule type: protein
A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 706-743,'R',745-812 <MAL>
A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasminogen #status experimental <PRO>
F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <MAT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;110-188/Domain: kringle homology <KR1>
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR5>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
 bonds: #status predicted
F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

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  Matches  185;  Conservative   72;  Mismatches  141;  Indels  38;  Gaps   11;

Qy         25 ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 84
                :|  |     : : || :|   :   | |:|| :    :||:    || :: | :    :
Db         42 SLSRKNLAGRSVEDCAAKC--EEETDFVCRAFQYHSKEQQCVVMAENSKNTPVFRM--RD 97

Qy         85 FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQEN 144
                 ||| : |:  |  | |::|:|| : ||||: || ||:  ||   | |  :    |:||
Db         98 VILYEKRIYLLECKTGNGQTYRGTTAETKSGVTCQKWSATSPHVPKFSPEKFPLAGLEEN 157

Qy        145 YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 204
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Db        158 YCRNPDNDENGPWCYTTDPDKRYDYCDIPEC-EDKCMHCSGENYEGKIAKTMSGRDCQAW 216

Qy        205 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMND 264

Db        217 DSQSPHAHGYIPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPQKRWEFCDIPRCT------ 270

Qy        265 TDVPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENY 322

Db        271 TPPPSSGPKYQCLKGTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENY 330

Qy        323 CRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH----------------GQDCYRGNG 365

Db        331 CRNPNGEKAPWCYTTNSEVRWEYCT-IPSCESSPLSTERMDVPVPPEQTPVPQDCYHGNG 389

Qy        366 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCY 422

Db        390 QSYRGTSSTTITGRKCQSWSSMTP--HRHLKTPENYPNAG-LTMNYCRNPDAD-KSPWCY 445

Qy        423 TGNPLIPWDYCPISRC 438

Db        446 TTDPRVRWEFCNLKKC 461


RESULT 15
T18518
apolipoprotein(a) - western European hedgehog (fragment)
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18518
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: T18518
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2869 <LAW>
A;Cross-references: UNIPROT:Q28398; EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC485
A;Experimental source: liver
C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con
ent apolipoprotein(a).

  Query Match             36.2%;  Score 943.5;  DB 2;  Length 2869;
  Best Local Similarity   45.6%;  Pred. No. 1.4e-58;
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Qy          89 ENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRN 148

Db        2490 EPLDLVDQCLEGTGENYRGNMAVTASGHTCQRWREQSPHSHSRTPENYPTKNLVGNYCRN 2549

Qy         149 PRGEEGGPWCFTSNPEVRYEVCDIPQCSE-----------VECMTCNGESYRGLMDHTES 197

Db        2550 PDGEV-APWCYTTNSAMRWEYCSIPACESPTPPTEHLVVPEQCLEGNGENYQGNMAITVS 2608

Qy         198 GKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC 257

Db        2609 GQPCQGWRKQTPHRHEYTPENYPSKNLFGNYCRNPDGEIAPWCYTTNSAVRWEYCSIPTC 2668

Qy         258 ADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKD 317

Db        2669 -ESSSPPTEPMIIPDQCLEGTGENYRGSVAVTVSGHTCQRWREQSPHSHSRTPENYPTKN 2727

Qy         318 LRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH-------GQD-CYRGNGKNYM 369

Db        2728 LFGNYCRNPDGEVAPWCYTTNSAVRWEYC-KIPSCNSSSSPTEPSTSQDQCLKGNGESYQ 2786

Qy         370 GNLSQTRSGLTCSMWDKNMEDLHRHIFWEPD---ASKLNENYCRNPDDDAHGPWCYTGNP 426

Db        2787 GNISVTVSGYTCQRWRE--QTPHRHA-RTPDNYPCKNLVGNYCRNPDGEV-APWCYTTNS 2842

Qy         427 LIPWDYCPISRCEGDTTPT 445

Db        2843 AVRWEYCSIPTCESPTPPT 2861


Search completed: October  3, 2005, 05:59:59
Job time : 41.225 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 65.3656 Seconds
(without alignments)
3501.834 Million cell updates/sec

Title: US-09-674-377B-1
Perfect score: 2604
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2601	99.9	728	1	HGF_HUMAN	P14210 homo sapien
2	2462	94.5	730	2	Q867B7	Q867b7 canis famil
3	2456	94.3	730	2	Q76BS1	Q76bs1 bos taurus
4	2452	94.2	728	2	Q9BH09	Q9bh09 felis silve
5	2409	92.5	728	2	Q8C9G5	Q8c9g5 mus musculu
6	2408	92.5	728	1	HGF_MOUSE	Q08048 mus musculu
7	2401	92.2	728	1	HGF_RAT	P17945 rattus norv
8	2052	78.8	726	2	Q90978	Q90978 gallus gall
9	1864.5	71.6	710	2	Q91402	Q91402 xenopus. he
10	1705.5	65.5	405	2	Q788Q2	Q788q2 gallus gall
11	1214	46.6	449	2	Q6GP14	Q6gp14 xenopus lae
12	1209.5	46.4	704	2	Q90865	Q90865 gallus gall
13	1208	46.4	716	2	Q91691	Q91691 xenopus lae
14	1180.5	45.3	711	1	HGFL_HUMAN	P26927 homo sapien
15	1176	45.2	717	2	P70006	P70006 xenopus lae
16	1172	45.0	709	2	Q90ZN6	Q90zn6 brachydanio
17	1168.5	44.9	709	2	Q7ZTN9	Q7ztn9 xenopus lae
18	1163.5	44.7	567	2	Q13208	Q13208 homo sapien
19	1144	43.9	716	2	P70521	P70521 rattus norv
20	1125	43.2	716	1	HGFL_MOUSE	P26928 mus musculu
21	1125	43.2	716	2	Q91XG8	Q91xg8 mus musculu
22	1089	41.8	818	2	Q6PBA6	Q6pba6 brachydanio
23	1085.5	41.7	812	1	PLMN_RAT	Q01177 rattus norv
24	1080.5	41.5	806	1	PLMN_MACEU	O18783 macropus eu
25	1066	40.9	790	1	PLMN_PIG	P06867 sus scrofa
26	1064	40.9	466	2	Q6TCI0	Q6tci0 mus musculu
27	1064	40.9	812	1	PLMN_MOUSE	P20918 mus musculu
28	1053.5	40.5	810	1	PLMN_ERIEU	Q29485 erinaceus e
29	1044.5	40.1	810	1	PLMN_MACMU	P12545 macaca mula
30	1042	40.0	810	1	PLMN_HUMAN	P00747 homo sapien
31	1040	39.9	215	2	O42341	O42341 gallus gall
32	1038	39.9	812	1	PLMN_BOVIN	P06868 bos taurus
33	1032.5	39.7	759	2	Q7TP84	Q7tp84 rattus norv
34	985	37.8	359	2	Q8WMR1	Q8wmr1 canis famil
35	966.5	37.1	648	2	Q9H1V4	Q9h1v4 homo sapien
36	943.5	36.2	2869	2	Q28398	Q28398 erinaceus e
37	896	34.4	211	2	O55027	O55027 mus musculu
38	879	33.8	4548	1	APOA_HUMAN	P08519 homo sapien
39	843.5	32.4	1420	1	APOA_MACMU	P14417 macaca mula
40	617	23.7	162	2	Q8C4E2	Q8c4e2 mus musculu
41	615	23.6	109	2	Q9N1B8	Q9n1b8 ovis aries
42	444.5	17.1	454	2	O46506	O46506 papio hamad
43	439	16.9	75	2	Q9BGN9	Q9bgn9 bos taurus
44	408.5	15.7	325	1	PLMN_PETMA	P33574 petromyzon
45	406	15.6	429	2	Q8AVB0	Q8avb0 brachydanio

ALIGNMENTS

RESULT 1
HGF_HUMAN
ID HGF_HUMAN STANDARD; PRT; 728 AA.
AC P14210; Q02935; Q13494; Q14519; Q8TCE2; Q9BYL9; Q9BYM0; Q9UDU6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoeitin A).
GN Name=HGF; Synonyms=HPTA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91340155; PubMed=1831432; DOI=10.1016/0378-1119(91)90080-U;
RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=89392017; PubMed=2528952;
RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
RA Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
RA Gohda E., Daikuhara Y., Kitamura N.;
RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT growth factor.";
RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Leukocyte;
RX MEDLINE=91025062; PubMed=2145836;
RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T., Asami O.,
RA Hagiya M., Nakamura T., Shimizu S.;
RT "Isolation and expression of cDNA for different forms of hepatocyte
RT growth factor from human leukocyte.";
RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 55-73 AND 495-520.
RC TISSUE=Liver;
RX MEDLINE=90066676; PubMed=2531289; DOI=10.1038/342440a0;
RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
RA Sugimura A., Tashiro K., Shimizu S.;
RT "Molecular cloning and expression of human hepatocyte growth factor.";
RL Nature 342:440-443(1989).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=91200041; PubMed=1826653;
RA Miyazawa K., Kitamura A., Naka D., Kitamura N.;
RT "An alternatively processed mRNA generated from human hepatocyte
RT growth factor gene.";

RL Eur. J. Biochem. 197:15-22(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 583-592.
RC TISSUE=Lung fibroblast;
RX PubMed=1824873;
RA Rubin J.S., Chan A.M.-L., Bottaro D.P., Burgess W.H., Taylor W.G.,
RA Cech A.C., Hirschfield D.W., Wong J., Miki T., Finch P.W.,
RA Aaronson S.A.;
RT "A broad-spectrum human lung fibroblast-derived mitogen is a variant
RT of hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:415-419(1991).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=91334393; PubMed=1831266;
RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
RA Rieder H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
RA Birchmeier W.;
RT "Evidence for the identity of human scatter factor and human
RT hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX PubMed=1720571;
RA Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid M.,
RA Aaronson S.A.;
RT "Identification of a competitive HGF antagonist encoded by an
RT alternative transcript.";
RL Science 254:1382-1385(1991).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND MUTAGENESIS OF ARG-494.
RX MEDLINE=93087571; PubMed=1280830;
RA Hartmann G., Naldini L., Weidner K.M., Sachs M., Vigna E.,
RA Comoglio P.M., Birchmeier W.;
RT "A functional domain in the heavy chain of scatter factor/hepatocyte
RT growth factor binds the c-Met receptor and induces cell dissociation
RT but not mitogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11574-11578(1992).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RX MEDLINE=96278713; PubMed=8662798; DOI=10.1074/jbc.271.22.13110;
RA Cioce V., Csaky K.G., Chan A.M.-L., Bottaro D.P., Taylor W.G.,
RA Jensen R., Aaronson S.A., Rubin J.S.;
RT "Hepatocyte growth factor (HGF)/NK1 is a naturally occurring
RT HGF/scatter factor variant with partial agonist/antagonist activity.";
RL J. Biol. Chem. 271:13110-13115(1996).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LYS-304 AND TYR-330.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [13]
RP SEQUENCE FROM N.A. (ISOFORMS 5 AND 6).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [14]
RP SEQUENCE OF 1-208 AND 249-695 FROM N.A. (ISOFORM 1).
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RT human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176(1991).
RN [15]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=91207365; PubMed=1826837;
RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
RA Hishida T., Daikuhara Y.;
RT "Identification of the N-terminal residue of the heavy chain of both
RT native and recombinant human hepatocyte growth factor.";
RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
RN [16]
RP CARBOHYDRATE-LINKAGE SITE THR-476.
RX MEDLINE=93129192; PubMed=1482348;
RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
RA Nakamura T., Shimizu S.;
RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
RT on the alpha chain.";
RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
RN [17]
RP MUTAGENESIS.
RX MEDLINE=92331602; PubMed=1321034;
RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
RA Baker J.B., Godowski P.J.;
RT "Structure-function analysis of hepatocyte growth factor:
RT identification of variants that lack mitogenic activity yet retain
RT high affinity receptor binding.";
RL EMBO J. 11:2503-2510(1992).
RN [18]
RP STRUCTURE BY NMR OF 31-127.
RX MEDLINE=98154323; PubMed=9493272; DOI=10.1016/S0969-2126(98)00012-4;
RA Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
RA Rubin J.S., Bottaro D.P., Byrd R.A.;
RT "The solution structure of the N-terminal domain of hepatocyte growth
RT factor reveals a potential heparin-binding site.";
RL Structure 6:109-116(1998).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.

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RX   MEDLINE=99036858; PubMed=9817840; DOI=10.1016/S0969-2126(98)00138-5;
RA   Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;

  Query Match             99.9%;  Score 2601;  DB 1;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-186;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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RESULT 2
Q867B7
ID   Q867B7      PRELIMINARY;      PRT;   730 AA.
AC   Q867B7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=HGF;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Beagle;
RX   MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1;
RA   Miyake M., Saze K., Yaguchi T., Wang J., Suzuta Y., Haga Y.,
RA   Takahashi S.Y., Yamamoto Y., Iwabuchi S.;
RT   "Canine hepatocyte growth factor: molecular cloning and
RT   characterization of the recombinant protein.";
RL   Vet. Immunol. Immunopathol. 95:135-143(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Liao A.T., Chien M.B., London C.A.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB090353; BAC57560.1; -.
DR   EMBL; AY543632; AAS48570.1; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.982; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   730 AA;  83398 MW;  4E83F9EA8BFF6DB1 CRC64;

  Query Match             94.5%;  Score 2462;  DB 2;  Length 730;
  Best Local Similarity   93.1%;  Pred. No. 2.9e-176;
  Matches  416;  Conservative   19;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKRCLWFPFNSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||| ||||||||||||||||||||||||||||||||||||||||:|||||
Db        212 MTCNGESYRGPMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | ||||||| || :||||||||:||||||||||||||:||||||:|||||||
Db        272 YTLDPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGTINTIWNGVPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:|||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        332 QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              |||||||||||||:||||||||:|||||||||||||||||||:|||||||||||||||||
Db        392 YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||| ||||||||||||
Db        452 CYTGNPLIPWDYCPIFRCEGDTTPTIV 478


RESULT 3
Q76BS1
ID   Q76BS1      PRELIMINARY;      PRT;   730 AA.
AC   Q76BS1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=hgf;
OS   Bos taurus (Bovine).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamaji D., Kimura K., Watanabe A., Makondo K., Saito M.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB110822; BAD02475.1; -.
DR   HSSP; P08519; 1KIV.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   730 AA;  83357 MW;  E39D653B0A85F49B CRC64;

  Query Match             94.3%;  Score 2456;  DB 2;  Length 730;
  Best Local Similarity   92.6%;  Pred. No. 8.2e-176;
  Matches  414;  Conservative   22;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||:|||||||| || |||||||:|||||||||| ||||||||||||||||
Db         32 QKKRRNTLHEFKRSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              |||:|||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         92 ARKRCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              |||||||||| |||||:||||||||||||||||||||||||||||||||:|||||
Db        212 MTCNGESYRGPMDHTETGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | ||||||| || :||||||:|::||||||||||||||:||||||||||||||
Db        272 YTLDPDTPWEYCAIKMCAHSTMNDTDLPMQTTECIQGQGEGYRGTINTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:|||||||||||||||:||||||||||||||||| ||:| ||||
Db        332 QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||:||:|||||||||||||||||||||||:|||:|||||||||||||||
Db        392 YRGNGKNYMGSLSKTRSGLTCSMWDKNMEDLHRHIFWEPDATKLNKNYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 4
Q9BH09
ID   Q9BH09      PRELIMINARY;      PRT;   728 AA.
AC   Q9BH09;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor HGF.
GN   Name=HGF;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Kobayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K.,
RA   Tsujimoto H.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Miyake M., Yaguchi T., Saze K., Suzuta Y., Wang J., Okazaki M.,
RA   Haga Y., Yamamoto Y., Takahashi S., Iwabuchi S.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB046610; BAB21499.1; -.
DR   EMBL; AB080187; BAC10545.1; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.982; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   728 AA;  83067 MW;  8D7F4A333D1E190A CRC64;

  Query Match             94.2%;  Score 2452;  DB 2;  Length 728;
  Best Local Similarity   92.6%;  Pred. No. 1.6e-175;
  Matches  414;  Conservative   21;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||| || |||||||:|||||||||| ||||||||||||||||
Db         30 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 89

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              |||:|||||||:|||||||||||||||||||||||||||| ||||||||||||||||
Db         90 ARKRCLWFPFNSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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                |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              |||||||||| |||||||||||||| |||||||||||||||||||||||||||||:|||||
Db        210 MTCNGESYRGPMDHTESGKICQRWDRQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 269

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | ||||||| || :||||||||:|||||||||||||||||:|:||||:|||||||
Db        270 YTLDPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGTINSIWNGVPCQRWDS 329

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:|||||||||||||:||||||:|||||||||||||||||||| ||:| ||||
Db        330 QYPHQHDITPENFKCKDLRENFCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 389

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              |||||||||||||:||||||||:|||||||||||||||||||:|||||||||||||||||
Db        390 YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 449

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476


RESULT 5
Q8C9G5
ID   Q8C9G5      PRELIMINARY;      PRT;   728 AA.
AC   Q8C9G5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A630060C16 product:hepatocyte growth factor, full
DE   insert sequence.
GN   Name=Hgf;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AK042121; BAC31175.1; -.
DR   HSSP; P14210; 1GMN.
DR   MGD; MGI:96079; Hgf.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   728 AA;  82990 MW;  8D5258DF3BCF3545 CRC64;

  Query Match             92.5%;  Score 2409;  DB 2;  Length 728;
  Best Local Similarity   91.1%;  Pred. No. 2.7e-172;
  Matches  407;  Conservative   21;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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                ||||||||||| |||||||| ||||| ||||||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
                ||||| | |||||||||| : :|:||||:|||||||||||||| ||||||||||||
Db        273 YTLDPDTTWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
                ||||:||:|||||||||||||||||||:|||||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
                |||||||||||||:|||||||||||||||||||||||||||||:|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                |||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479


RESULT 6
HGF_MOUSE
ID   HGF_MOUSE      STANDARD;      PRT;   728 AA.
AC   Q08048; Q61662; Q64007;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor precursor (Scatter factor) (SF)
DE   (Hepatopoeitin A).
GN   Name=Hgf;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
RC   TISSUE=Mammary fibroblast;
RX   MEDLINE=94183257; PubMed=8135822;
RA   Sasaki M., Nishio M., Sasaki T., Enami J.;
RT   "Identification of mouse mammary fibroblast-derived mammary growth
RT   factor as hepatocyte growth factor.";
RL   Biochem. Biophys. Res. Commun. 199:772-779(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94363381; PubMed=8081873;
RA   Lee C.C., Kozak C.A., Yamada K.M.;
RT   "Structure, genetic mapping, and expression of the mouse Hgf/scatter
RT   factor gene.";
RL   Cell Adhes. Commun. 1:101-111(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B;
RA   Liu Y., Michalopoulos G.K., Zarnegar R.;
RT   "Molecular cloning and characterization of cDNA encoding mouse
RT   hepatocyte growth factor.";
RL   Biochim. Biophys. Acta 1216:299-303(1993).
CC   -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC       hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC       growth factor for a broad spectrum of tissues and cell types. It
CC       has no detectable protease activity.
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC       disulfide bond.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=Q08048-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=Q08048-2; Sequence=VSP_005408;
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC       subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10212; BAA01064.1; -.
DR   EMBL; D10213; BAA01065.1; -.
DR   EMBL; S71816; AAB31855.1; -.
DR   EMBL; X72307; CAA51054.1; ALT_INIT.
DR   PIR; JC2117; A60185.
DR   HSSP; P14210; 1BHT.
DR   MEROPS; S01.982; -.
DR   MGD; MGI:96079; Hgf.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Growth factor; Kringle; Pyrrolidone carboxylic acid; Repeat;
KW   Serine protease homolog; Signal.
FT   SIGNAL       1     32       By similarity.
FT   CHAIN       33    495       Hepatocyte growth factor alpha chain.
FT   CHAIN      496    728       Hepatocyte growth factor beta chain.
FT   MOD_RES      33     33       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DOMAIN       38    124       PAN.
FT   DOMAIN      129    207       Kringle 1.
FT   DOMAIN      212    289       Kringle 2.
FT   DOMAIN      306    384       Kringle 3.
FT   DOMAIN      392    470       Kringle 4.
FT   DOMAIN      496    728       Serine protease-like.
FT   DISULFID     71     97       By similarity.
FT   DISULFID     75     85       By similarity.
FT   DISULFID    488    607       Interchain (By similarity).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    403    403       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    569    569       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    656    656       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    163    167       Missing (in isoform Short).
FT                                /FTId=VSP_005408.
FT   CONFLICT    344    344       N -> K (in Ref. 2).
FT   CONFLICT    479    479       V -> L (in Ref. 2).
FT   CONFLICT    564    564       R -> H (in Ref. 3).
SQ   SEQUENCE   728 AA;  82944 MW;  A0381FC497534328 CRC64;

  Query Match             92.5%;  Score 2408;  DB 1;  Length 728;
  Best Local Similarity   91.1%;  Pred. No. 3.2e-172;
  Matches  407;  Conservative   21;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
```

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                ::|||||:|||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
                :||:| |:|||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
                |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
                |||||||||| |||||||| ||||| ||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
                ||||| | |||||||||| : :|:||||:|||||||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
                ||||:||:|||||||||||||||||:|||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
                ||||||||||||:|||||||||||||||||||||||||:||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
                |||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479
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RESULT 7
HGF_RAT
ID   HGF_RAT   STANDARD;   PRT;   728 AA.
AC   P17945;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor precursor (Scatter factor) (SF)
DE   (Hepatopoeitin A).
GN   Name=Hgf;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=90222197; PubMed=2139229;
RA   Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
RA   Shimizu S., Nakamura T.;
RT   "Deduced primary structure of rat hepatocyte growth factor and
RT   expression of the mRNA in rat tissues.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=91031482; PubMed=2146117;
RA   Okajima A., Miyazawa K., Kitamura N.;
RT   "Primary structure of rat hepatocyte growth factor and induction of
RT   its mRNA during liver regeneration following hepatic injury.";
RL   Eur. J. Biochem. 193:375-381(1990).
CC   -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC   hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC   growth factor for a broad spectrum of tissues and cell types. It
CC   has no detectable protease activity.
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC   disulfide bond.
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC   subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; D90102; BAA14133.1; -.
DR   EMBL; X54400; CAA38266.1; -.
DR   PIR; A35644; A35644.
DR   HSSP; P14210; 1BHT.
DR   MEROPS; S01.978; -.
DR   RGD; 2794; Hgf.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Direct protein sequencing; Glycoprotein; Growth factor; Kringle;
KW   Pyrrolidone carboxylic acid; Repeat; Serine protease homolog; Signal.
FT   SIGNAL   1   32   By similarity.
FT   CHAIN   33   495   Hepatocyte growth factor alpha chain.
FT   CHAIN   496   728   Hepatocyte growth factor beta chain.
FT   MOD_RES   33   33   Pyrrolidone carboxylic acid (By
FT   similarity).
FT   DOMAIN   38   124   PAN.
FT   DOMAIN   129   207   Kringle 1.
FT   DOMAIN   212   289   Kringle 2.
FT   DOMAIN   306   384   Kringle 3.
FT   DOMAIN   392   470   Kringle 4.
FT   DOMAIN   496   728   Serine protease-like.
FT   DISULFID   71   97   By similarity.
FT   DISULFID   75   85   By similarity.
FT   DISULFID   488   607   Interchain (By similarity).
FT   CARBOHYD   295   295   N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   403   403   N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   569   569   N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   656   656   N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   728 AA; 82905 MW; 3E0BF1F96ADCEDFF CRC64;

  Query Match   92.2%; Score 2401; DB 1; Length 728;
  Best Local Similarity   90.4%; Pred. No. 1.1e-171;
  Matches 404; Conservative   23; Mismatches   20; Indels   0; Gaps   0;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
                ::|||||:|||||||||||| | || :|||||||||:||:||||| |||| ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLVKIKTKKVNSADECANRCIRNKGFPFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
                :||:| |:|||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
                |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212
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Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||| |||||||| ||||| ||||||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||| | ||||||| || : :|:||||:|||||:||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKMCAHSAVNETDVPMETTECIKGQGEGYRGTTNTIWNGIPCQRWDS 332

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||:||:||||||||||||||||||:||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              |||||||||||||:|||||||||||||||||||||||||||| :|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLTKNYCRNPDDDAHGPW 452

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||:|||||||||||||||||||
Db        453 CYTGNPLVPWDYCPISRCEGDTTPTIV 479


RESULT 8
Q90978
ID   Q90978      PRELIMINARY;      PRT;   726 AA.
AC   Q90978; Q90866;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor /scatter factor.
GN   Name=HGF/SF;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96029010; PubMed=7554499;
RA   Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
RT   "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions
RT   during early chick development.";
RL   Dev. Genet. 17:90-101(1995).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; X84045; CAA58864.1; -.
DR   PIR; I51285; I51285.
DR   HSSP; P14210; 1GMN.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   726 AA;  82865 MW;  5BD06CFB5C40B003 CRC64;

  Query Match           78.8%;  Score 2052;  DB 2;  Length 726;
  Best Local Similarity   76.6%;  Pred. No. 1.6e-145;
  Matches  341;  Conservative   49;  Mismatches   53;  Indels    2;  Gaps    1;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:||||| |||||| :|:

Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:||||||  ||||:||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 182
              ||||||||||||||||||:|||||||||||||||||::|:|:|:|||||| ||||||||
Db        150 SMIPHEHSFLPSSYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMT 209

Qy        183 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 242
              |||||||| |||||||| ||||| | ||:||| ||||||||||||||||||: ||||||
Db        210 CNGESYRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYT 269

Qy        243 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 302
              |||:| ||:|||||    :| |:   ||| ||||||||||||||||:|| |||||||:
Db        270 LDPNTPWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQF 329

Qy        303 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 362
              ||:|::|||||||||||||||||||||||||||||||:||||||| ||:|: |||||
Db        330 PHQHNITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYR 389

Qy        363 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRH--IFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||:|||||| || ||||| ||||:||| ||  || ||| ||| :|||||||| ||||
Db        390 GNGKSYMGNLSNTRIGLTCSTWDKNIEDLRRHIQIFREPDVSKLKKNYCRNPDDDFHGPW 449

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPT 445
              ||| :|||||||||||| ||||||
Db        450 CYTDDPLIPWDYCPISRCTGDTTPT 474


RESULT 9
Q91402
ID   Q91402      PRELIMINARY;      PRT;   710 AA.
AC   Q91402;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=HGF;
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tailbud;
RX   MEDLINE=95267690; PubMed=7748783; DOI=10.1016/0925-4773(94)00309-B;
RA   Nakamura H., Tashiro K., Nakamura T., Shiokawa K.;
RT   "Molecular cloning of Xenopus HGF cDNA and its expression studies in
RT   Xenopus early embryogenesis.";
RL   Mech. Dev. 49:123-131(1995).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; S77422; AAB34354.2; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.976; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
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DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   710 AA;  81487 MW;  5FE6480BE31C27FC CRC64;

  Query Match             71.6%;  Score 1864.5;  DB 2;  Length 710;
  Best Local Similarity   69.3%;  Pred. No. 1.8e-131;
  Matches  305;  Conservative   64;  Mismatches   68;  Indels    3;  Gaps    1;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |:||   ::||:|:||| ::: ||::|||  || : || ||:||||||||||||| |||
Db         21 KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI 80

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| || ||:||:|:| ::   ||||| |||||:|| ||| :|:|| ::|| |: ||||:
Db         81 KRCHWFSFNTMSAGIKDKYDISFDLYEKKDYIRDCIHGKGSNYRGTRNVTKRGLACQPWN 140

Qy        123 SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 182
              |||||||||||:|||||:|||||||:|||||||||| :||||::||||| ||||:|:|
Db        141 SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT 200

Qy        183 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 242
              |||| ||| ||:||||| ||||| | ||:||| |||||:|| :|||||||: ||||||
Db        201 CNGEHYRGPMDYTESGKECQRWDLQRPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT 260

Qy        243 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 302
              ||| | ||:|||| |  : :|:||:   | :|::||||||||:|:| :||| |||||||:
Db        261 LDPDTSWEFCAIKPCVHSIVNNTDI---TKDCMKGQGEGYRGSVSTTYNGIQCQRWDSQF 317

Qy        303 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 362
              || |: ||||:||||| |||||||||||||||||||||:|:|||| | |: |:||
Db        318 PHLHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY 377

Qy        363 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY 422
              |||  | | ||:||  | ||||:||::|| || | ||| | | :|||||||:||||||||
Db        378 GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY 437

Qy        423 TGNPLIPWDYCPISRCEGDT 442
              | :| :|||||||||||||
Db        438 TDDPFVPWDYCPISRCEGDT 457


RESULT 10
Q788Q2
ID   Q788Q2      PRELIMINARY;      PRT;   405 AA.
AC   Q788Q2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HGF/SF protein precursor (Fragment).
GN   Name=HGF/SF;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95237013; PubMed=7720585;
RA   Streit A., Stern C.D., Thery C., Ireland G.W., Aparicio S.,
RA   Sharpe M.J., Gherardi E.;
RT   "A role for HGF/SF in neural induction and its expression in Hensen's
RT   node during gastrulation.";
RL   Development 121:813-824(1995).
DR   EMBL; X80131; CAA56430.1; -.
DR   HSSP; P00747; 1KI0.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 3.
DR   SMART; SM00130; KR; 3.
DR   SMART; SM00473; PAN_AP; 1.
DR   PROSITE; PS00021; KRINGLE_1; 3.
DR   PROSITE; PS50070; KRINGLE_2; 3.
DR   PROSITE; PS50948; PAN; 1.
KW   Kringle; Signal.
FT   SIGNAL       1     25       Potential.
FT   NON_TER     405    405
SQ   SEQUENCE   405 AA;  46550 MW;  EB7BAD4EF220B449 CRC64;

  Query Match             65.5%;  Score 1705.5;  DB 2;  Length 405;
  Best Local Similarity   74.7%;  Pred. No. 8.3e-120;
  Matches  284;  Conservative   47;  Mismatches   44;  Indels    5;  Gaps    1;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:||||| |||||| :|:
Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:||||||||  ||||:|||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 182
              |||||||     |||||||:||||||||||||||||::|::|:|||||| ||||||||
Db        150 SMIPHEH-----SYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMT 204

Qy        183 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 242
              |||||||| |||||||| ||||| | ||:||| |||||||||||||||||||: ||||||
Db        205 CNGESYRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYT 264

Qy        243 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 302
              |||:| ||:||||||    :| |:   ||| ||||||||||||||||:|| |||||||:
Db        265 LDPNTPWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQF 324

Qy        303 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 362
              ||:|::|||||||||||||||||||||||||||||||:||||||| ||:|: |||||
Db        325 PHQHNITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYR 384

Qy        363 GNGKNYMGNLSQTRSGLTCS 382
              ||||:||||||:|| |||||
Db        385 GNGKSYMGNLSKTRFGLTCS 404


RESULT 11
Q6GP14
ID   Q6GP14      PRELIMINARY;      PRT;   449 AA.
AC   Q6GP14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC397993 protein.
GN   Name=LOC397993;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073334; AAH73334.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
KW   Kringle.
SQ   SEQUENCE   449 AA;  52467 MW;  5C2CE4B708E13D0B CRC64;

  Query Match             46.6%;  Score 1214;  DB 2;  Length 449;
  Best Local Similarity   47.3%;  Pred. No. 6.8e-83;
  Matches  207;  Conservative   74;  Mismatches  145;  Indels   12;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: ::::::|    |: ::    :| :  :    || :|:        |::||::   :
Db         21 RSALNDYQRSKGLELVHMNNG-GVKQEIQSEIQVCAKQCSD----LLDCRSFVYNWKSQS 75

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
              |   |:   |: |  :   ::|||: |||||:|::| | :|:|||| ||||  || |
Db         76 CRLLPWTQNSANVLLQRNVQYDLYQKKDYIRDCVVGNGNTYRGTVSKTKSGRTCQRWRLK 135

Qy        125 IPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCN 184
               ||:| | |  :   ||:|||||||  :  ||||:|::  :|:: | | :| :  |:|||
Db        136 FPHDHKFSPIHW--PDLEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCN 193

Qy        185 GESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLD 244
              || ||| :| ||||| ||||| |||| | : ||:|||| |||||||||   |||||| |
Db        194 GEDYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTD 253

Qy        245 PHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPH 304
              |:   |:| |  |    ::: ::   |: | : :|||||  ||  :|||||||||| |
Db        254 PNVEKEFCRITKCKKQRLSNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDSQTPQ 310

Qy        305 EHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRG 363
              |  || : || | ||||||||||:|||||| | :|: || ||  | |     ||| |
Db        311 SHRFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHG 370

Qy        364 NGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYT 423
              ||: | | :|:|| |: |  |::   ||   :  :|    | |||||||| |:|||||||
Db        371 NGELYSGRVSKTRKGIKCRRWEEKRNDLELSLD-QPYLVPLEENYCRNPDRDSHGPWCYT 429

Qy        424 GNPLIPWDYCPISRCEGD 441
               :|  |:||| |  |||:
Db        430 MDPNTPFDYCAIKPCEGE 447


RESULT 12
Q90865
ID   Q90865      PRELIMINARY;      PRT;   704 AA.
AC   Q90865;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor-like/macrophage stimulating protein.
GN   Name=HGF1/MSP;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=96029010; PubMed=7554499;
RA   Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
RT   "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions
RT   during early chick development.";
RL   Dev. Genet. 17:90-101(1995).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; X84043; CAA58862.1; -.
DR   HSSP; P00747; 1CEA.
DR   MEROPS; S01.977; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   704 AA;  79341 MW;  CAB0D8CC41367C37 CRC64;

  Query Match             46.4%;  Score 1209.5;  DB 2;  Length 704;
  Best Local Similarity   46.0%;  Pred. No. 2.4e-82;
  Matches  207;  Conservative   71;  Mismatches  149;  Indels   23;  Gaps    8;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: :::|::   | |                | ||| ||       |:||  ::  :
Db         20 RSPLNDFQRLRGTELRAAPNEPPPSAPAHGAAQQCAQRCANRP----DCRAFHHERQSQL 75

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
              |   |::  | | : :    :|||: ||::| ||:  | ||:||   |: |::|| | :
Db         76 CQLLPWSQRSPGARLQKNIHYDLYQKKDFLRECIVANGTSYRGTRDTTERGLRCQHWQAT 135

Qy        125 IPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCN 184
               ||:| ||||    |  |:|||||||  :: ||||:| :| ||:: | | :| :  |||||
Db        136 TPHDHRFLPSLRNG--LEENYCRNPDRDKRGPWCYTVDPNVRHQSCGIKKCEDAVCMTCN 193

Qy        185 GESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLD 244
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Db        194 GEDYRGFVDHTESGTECQRWDLQHPHKHPYHPDKYPEKGLDDNYCRNPDSSEQPWCYTTD 253

Qy        245 PHTRWEYCAIKTCADNTMNDTDVPLE-TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYP 303

Db        254 PALEREFCRIRVCKKRPR-----PINVTTGCYRGKGEGYRGRVNVTVSGIPCQRWDAQTL 308

Qy        304 HEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMS-HGQDCYR 362

Db        309 HRHHFVPSKYPCKDLQENYCRNPDGSEAPWCFTTRPGMRVAFCFHIRRCDDELDAEECYH 368

Qy        363 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI-----FWEPDASKLNENYCRNPDDDAH 417

Db        369 GHGERYHGHVSKTRKGITCQRWDATTP----HVPQISPTTHPEA-HLEKNYCRNPDNDSH 423

Qy        418 GPWCYTGNPLIPWDYCPISRCEGDTTPTIV 447

Db        424 GPWCYTMDPRTPFDYCAIKPCSGSAVPSVL 453


RESULT 13
Q91691
ID   Q91691      PRELIMINARY;      PRT;   716 AA.
AC   Q91691;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Growth factor Livertine.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ruiz i Altaba A., Thery C.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U57455; AAB52574.1; -.
DR   HSSP; P00746; 1FDP.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   716 AA;  81971 MW;  508376A0E4398798 CRC64;

  Query Match             46.4%;  Score 1208;  DB 2;  Length 716;
  Best Local Similarity   46.7%;  Pred. No. 3.2e-82;
  Matches  207;  Conservative   75;  Mismatches  149;  Indels   12;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64

Db         31 RSALNDYQRSKGLELVHMNNG-GVKQEIQSEIQVCAKQCSD----LLDCRSFVYNWKSQT 85

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124

Db         86 CRLLPWTQNSANVLLQRNVQYDLYQKKDYIRDCVAGNGNTYRGTVSKTKSGRTCQRWRLK 145

Qy        125 IPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCN 184

Db        146 FPHDHKFSPIHW--PELEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCN 203

Qy        185 GESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLD 244

Db        204 GEDYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTD 263

Qy        245 PHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPH 304

Db        264 PNVEKEFCRITKCKKQRLSNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDSQTPQ 320

Qy        305 EHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRG 363

Db        321 SHRFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHG 380

Qy        364 NGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYT 423

Db        381 NGELYSGRVSKTRKGIKCRRWEEKRNDLELSLD-QPYLVPLEENYCRNPDRDSHGPWCYT 439

Qy        424 GNPLIPWDYCPISRCEGDTTPTI 446

Db        440 MDPNTPFDYCAIKPCEGEKVLTL 462


RESULT 14
HGFL_HUMAN
ID   HGFL_HUMAN     STANDARD;      PRT;   711 AA.
AC   P26927; Q13350; Q14870;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor-like protein precursor (Macrophage
DE   stimulatory protein) (MSP) (Macrophage stimulating protein).
GN   Name=MST1; Synonyms=HGFL;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=92002016; PubMed=1655021;
RA   Han S., Stuart L.A., Friezner Degen S.J.;
RT   "Characterization of the DNF15S2 locus on human chromosome 3:
RT   identification of a gene coding for four kringle domains with homology
RT   to hepatocyte growth factor.";
RL   Biochemistry 30:9768-9780(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93340141; PubMed=8393443;
RA   Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
RT   "Cloning, sequencing, and expression of human macrophage stimulating
RT   protein (MSP, MST1) confirms MSP as a member of the family of kringle
RT   proteins and locates the MSP gene on chromosome 3.";
RL   J. Biol. Chem. 268:15461-15468(1993).
RN   [3]
RP   SEQUENCE OF 230-247; 288-310; 326-341; 484-501; 530-549; 574-596 AND
RP   602-611, AND SUBUNIT.
RC   TISSUE=Plasma;
RX   PubMed=1827141;
RA   Skeel A., Yoshimura T., Showalter S.D., Tanaka S., Appella E.,
RA   Leonard E.J.;
RT   "Macrophage stimulating protein: purification, partial amino acid
RT   sequence, and cellular activity.";
RL   J. Exp. Med. 173:1227-1234(1991).
CC   -!- FUNCTION: Probably has no proteolytic activity, since crucial AA
CC       characteristic of serine proteases catalytic sites are not
CC       conserved.
```

```
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC       disulfide bond.
CC   -!- PTM: May be cleaved after Arg-483, to yield two chains held
CC       together by disulfide bonds, or two separate polypeptides.
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC       subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74178; AAA50165.1; -.
DR   EMBL; U37055; AAC50471.1; -.
DR   EMBL; L11924; AAA59872.1; -.
DR   PIR; A40331; A47136.
DR   HSSP; P00766; 1CHG.
DR   MEROPS; S01.975; -.
DR   Genew; HGNC:7380; MST1.
DR   MIM; 142408; -.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Direct protein sequencing; Glycoprotein; Kringle; Polymorphism;
KW   Repeat; Serine protease homolog; Signal.
FT   SIGNAL       1     18       Potential.
FT   CHAIN       19    711       Hepatocyte growth factor-like protein.
FT   DOMAIN      21    105       PAN.
FT   DOMAIN     110    186       Kringle 1.
FT   DOMAIN     191    268       Kringle 2.
FT   DOMAIN     283    361       Kringle 3.
FT   DOMAIN     370    448       Kringle 4.
FT   DOMAIN     484    711       Serine protease-like.
FT   DISULFID    56     78       By similarity.
FT   DISULFID    60     66       By similarity.
FT   DISULFID   110    186       By similarity.
FT   DISULFID   131    169       By similarity.
FT   DISULFID   157    181       By similarity.
FT   DISULFID   191    268       By similarity.
FT   DISULFID   194    324       Interchain (By similarity).
FT   DISULFID   212    251       By similarity.
FT   DISULFID   240    263       By similarity.
FT   DISULFID   283    361       By similarity.
FT   DISULFID   304    343       By similarity.
FT   DISULFID   332    355       By similarity.
FT   DISULFID   370    448       By similarity.
FT   DISULFID   391    431       By similarity.
FT   DISULFID   419    443       By similarity.
FT   DISULFID   468    588       Interchain (By similarity).
FT   DISULFID   507    523       By similarity.
FT   DISULFID   602    667       By similarity.
FT   DISULFID   632    646       By similarity.
FT   DISULFID   657    685       By similarity.
FT   CARBOHYD    72     72       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   615    615       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT     13     13       Y -> C.
FT                               /FTId=VAR_006631.
FT   VARIANT    212    212       C -> F.
FT                               /FTId=VAR_006632.
FT   VARIANT    676    676       E -> K (in dbSNP:7798).
FT                               /FTId=VAR_014569.
FT   CONFLICT   292    292       R -> G (in Ref. 3).
FT   CONFLICT   304    304       C -> E (in Ref. 3).
FT   CONFLICT   306    306       R -> E (in Ref. 3).
FT   CONFLICT   550    551       PS -> SL (in Ref. 3).
FT   CONFLICT   593    593       W -> E (in Ref. 3).
FT   CONFLICT   623    623       L -> F (in Ref. 2).
SQ   SEQUENCE   711 AA;  80379 MW;  596ED21F180290E4 CRC64;

  Query Match             45.3%;  Score 1180.5;  DB 1;  Length 711;
  Best Local Similarity   47.4%;  Pred. No. 3.7e-80;
  Matches  197;  Conservative   62;  Mismatches  148;  Indels    9;  Gaps    4;

Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
              |  |::|| ||    |    |:|| :: :   |   |:   |   :       ||:: ||
Db         50 VADAEECAGRC----GPLMDCRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE 152
              |:| ||:  |  |:||::  |  |: || ||   |::| : |:   |  |:||:|||| |:
Db        106 YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNG--LEENFCRNPDGD 163

Qy        153 EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH 212
              |||||:|::| ||:: | |  | |  |: |||| ||| :| ||||: ||||| | ||:|
Db        164 PGGPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQH 223

Qy        213 KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETT 272
              | | :: |:| ||||||||||  |||||| ||    |:| :  |        :    |
Db        224 PFEPGKFLDQGLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTV 281

Qy        273 ECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESP 332
              | :|:|||||| ||   |:|||||:| ||:|  ||| : |||||||:||||||:|
Db        282 SCFRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAP 341

Qy        333 WCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDL 391
              ||||  | :|  :| ||  | |    |||| | |: | | :|:|| |: |  |
Db        342 WCFTLRPGMRAAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQCQRWSAETPHK 401

Qy        392 HRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV 447
              :  |     ::| ||:|||||  |:|||||| :|  |:||| : ||  |  |:|:
Db        402 PQFTFTSEPHAQLEENFCRNPDGDSHGPWCYTMDPRTPFDYCALRRCADDQPPSIL 457


RESULT 15
P70006
ID   P70006      PRELIMINARY;      PRT;   717 AA.
AC   P70006;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor-like protein precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96404125; PubMed=8808403; DOI=10.1016/0925-4773(95)00458-0;
RA   Aberger F., Schmidt G., Richter K.;
RT   "The Xenopus homologue of hepatocyte growth factor-like protein is
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RT   specifically expressed in the presumptive neural plate during
RT   gastrulation.";
RL   Mech. Dev. 54:23-37(1996).
DR   EMBL; Y08734; CAA69989.1; -.
DR   HSSP; P00746; 1FDP.
DR   MEROPS; S01.977; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease; Signal.
FT   SIGNAL        1     29       Potential.
FT   CHAIN        29    717       hepatocyte growth factor-like protein.
SQ   SEQUENCE   717 AA;  82017 MW;  6F877A432C8CDD54 CRC64;

  Query Match             45.2%;  Score 1176;  DB 2;  Length 717;
  Best Local Similarity   45.4%;  Pred. No. 8.1e-80;
  Matches  201;  Conservative   78;  Mismatches  152;  Indels   12;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: ::::::|    |: ::    :| :       || :|:       |::| ::   :
Db         32 RSALNDYQRSKGLELVHMNEG-GVKQEVQAEIQICAKQCSD----LLDCRSFDYNWKSQS 86

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
              |   |:   || |  :   ::|||: |||||:|::| | :|:|||| ||:|  || |
Db         87 CRLLPWTQNSSNVLLQRNVQYDLYQKKDYIRDCVVGNGNTYRGTVSKTKNGRTCQHWRLK 146

Qy        125 IPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCN 184
               ||:| | |: :   :|:|||||||  :  | ||:|::  :|:: | | :| :  |:|||
Db        147 FPHDHKFSPTHW--PELEENYCRNPDSDPEGLWCYTTDKNIRHQYCGIKKCEDAVCLTCN 204

Qy        185 GESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLD 244
              || ||| :| ||||| ||||| | || | : ||:|||| |||||||||   |||||| |
Db        205 GEDYRGSVDRTESGKECQRWDLQAPHTHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTD 264

Qy        245 PHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPH 304
              |:   |:| |  |    ::: ::   |: | : :||||||  ||  :||||||||:| ||
Db        265 PNVEREFCHITKCKKQRISNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDTQAPH 321

Qy        305 EHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRG 363
               |   || : || | ||||||| |||:|||||  |:|: || ||  | |     :|| |
Db        322 VHRFLPEKYPCKGLDENYCRNPVGSEAPWCFTTLKNMRMAYCFQIKRCTDDVVEPECYHG 381

Qy        364 NGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYT 423
              ||: | | :|:|| |: |  |::   ||   :  :|    | |||||||| |:|||||||
Db        382 NGELYRGRVSKTRKGIMCRRWEEKQNDLELSLA-QPYLVPLEENYCRNPDRDSHGPWCYT 440

Qy        424 GNPLIPWDYCPISRCEGDTTPTI 446
              :|  |:||| :  | ||   |:
Db        441 MDPNTPFDYCALKPCAGDKVLTL 463

Search completed: October  3, 2005, 06:08:09
Job time : 69.3656 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 172.465 Seconds
(without alignments)
1002.420 Million cell updates/sec

Title: US-09-674-377B-1
Perfect score: 2604
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2601	99.9	447	7	ADE37393	Ade37393 Human hep
2	2601	99.9	447	7	ADM83266	Adm83266 Human NK4
3	2601	99.9	697	3	AAY98485	Aay98485 Hepatocyt
4	2601	99.9	697	3	AAY59030	Aay59030 Sequence
5	2601	99.9	697	4	AAB45838	Aab45838 Nucleic a
6	2601	99.9	697	4	AAU04275	Aau04275 Nuclear l
7	2601	99.9	728	2	AAR25676	Aar25676 Recombina
8	2601	99.9	728	2	AAR20005	Aar20005 Human hep
9	2601	99.9	728	2	AAR40862	Aar40862 Competati
10	2601	99.9	728	2	AAR40863	Aar40863 Competati
11	2601	99.9	728	2	AAR42062	Aar42062 Vascular
12	2601	99.9	728	2	AAR87522	Aar87522 Mutant he
13	2601	99.9	728	2	AAR87524	Aar87524 Mutant he
14	2601	99.9	728	2	AAR87525	Aar87525 Mutant he
15	2601	99.9	728	2	AAR87523	Aar87523 Mutant he
16	2601	99.9	728	2	AAW00340	Aaw00340 Wild type
17	2601	99.9	728	2	AAW00338	Aaw00338 Human hep
18	2601	99.9	728	2	AAW59922	Aaw59922 Human leu
19	2601	99.9	728	2	AAW58696	Aaw58696 Human hep
20	2601	99.9	728	2	AAW42998	Aaw42998 Recombina
21	2601	99.9	728	2	AAW39207	Aaw39207 Human hep
22	2601	99.9	728	6	ABP58128	Abp58128 Human hep
23	2601	99.9	728	7	ADB61534	Adb61534 Hepatocyt
24	2601	99.9	728	8	ADM97652	Adm97652 Human hep
25	2601	99.9	728	8	ADT89322	Adt89322 Human hep
26	2601	99.9	951	8	ADS19044	Ads19044 Chimeric
27	2599	99.8	447	3	AAY57173	Aay57173 N-termina
28	2595	99.7	727	2	AAR10656	Aar10656 Hepatic p
29	2595	99.7	728	2	AAR15623	Aar15623 Human leu
30	2595	99.7	728	2	AAR14243	Aar14243 Human hep
31	2595	99.7	728	2	AAR39521	Aar39521 Hepatocyt
32	2591	99.5	728	2	AAW88529	Aaw88529 Human hep
33	2588	99.4	728	2	AAW88532	Aaw88532 Human hep
34	2587	99.3	728	2	AAW88531	Aaw88531 Human hep
35	2586	99.3	728	2	AAW88530	Aaw88530 Human hep
36	2577	99.0	728	2	AAR47227	Aar47227 Hepatocyt
37	2565	98.5	728	2	AAR12792	Aar12792 Human hep
38	2565	98.5	728	2	AAR52941	Aar52941 Human hep
39	2565	98.5	728	2	AAR52942	Aar52942 Human hep
40	2565	98.5	728	2	AAR52945	Aar52945 Human hep
41	2565	98.5	728	2	AAR52947	Aar52947 Human hep
42	2565	98.5	728	2	AAR52944	Aar52944 Human hep
43	2565	98.5	728	2	AAR52948	Aar52948 Human hep
44	2565	98.5	728	2	AAR52940	Aar52940 Human hep
45	2565	98.5	728	2	AAR52943	Aar52943 Human hep

ALIGNMENTS

RESULT 1
ADE37393
ID ADE37393 standard; protein; 447 AA.
XX
AC ADE37393;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human hepatocyte growth factor N-terminal four kringle fragment.
XX
KW conjugate; HGF/SF; hairpin domain; kringle region; PEG group; cancer;
KW human;
KW hepatocyte growth factor N-terminal four kringle-containing fragment;
KW NK4.
XX
OS Homo sapiens.
XX
PN EP1234583-A1.
XX
PD 28-AUG-2002.
XX
PF 23-FEB-2001; 2001EP-00104640.
XX
PR 23-FEB-2001; 2001EP-00104640.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
DR WPI; 2003-749561/71.
DR N-PSDB; ADE37392.
XX
PT Conjugate comprises an N-terminal fragment of hepatocyte growth factor
PT consisting of the hairpin domain and the four kringle regions of the
PT alpha-chain and one to three polyethylene glycol groups, useful for
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 2; 25pp; English.
XX
CC The invention comprises a conjugate that contains an N-terminal fragment
CC of hepatocyte growth factor (HGF/SF) consisting of the hairpin domain and
CC the four kringle regions of the alpha-chain and 1-3 polyethylene glycol
CC (PEG) groups. The conjugate of the invention is useful for the
CC preparation of a medicament for the treatment of cancer. The present
CC amino acid sequence represents the human N-terminal four kringle-
CC containing fragment of hepatocyte growth factor (NK4).
XX
SQ Sequence 447 AA;

Query Match 99.9%; Score 2601; DB 7; Length 447;

```
  Best Local Similarity   99.8%;  Pred. No. 5.5e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 2
ADM83266
ID   ADM83266 standard; protein; 447 AA.
XX
AC   ADM83266;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human NK4 protein #1.
XX
KW   NK4 gene; neovascularisation; ovarian cancer; pancreatic cancer;
KW   stomach cancer; gallbladder cancer; renal cancer; prostatic cancer;
KW   breast cancer; esophageal cancer; hepatic cancer; oral cavity cancer;
KW   colon cancer; colorectal cancer; sarcoma; glioma; melanoma; gene therapy;
KW   human.
XX
OS   Homo sapiens.
XX
PN   US2003162736-A1.
XX
PD   28-AUG-2003.
XX
PF   27-SEP-2002; 2002US-00255649.
XX
PR   25-FEB-2002; 2002JP-00048644.
XX
PA   (NAKA/) NAKAMURA T.
PA   (MATS/) MATSUMOTO K.
XX
PI   Nakamura T,  Matsumoto K;
XX
DR   WPI; 2003-897946/82.
DR   N-PSDB; ADM83264.
XX
PT   New NK14 gene, useful for producing a medicament for preventing or
PT   treating diseases caused by neovascularization, e.g. cancer.
XX
PS   Disclosure; Page 15-17; 27pp; English.
XX
CC   The present invention provides a therapeutic agent NK4 polypeptides and
CC   their encoding polynucleotides. The invention is useful for producing a
CC   medicament for preventing or treating diseases caused by
CC   neovascularisation such as ovarian cancer, pancreatic cancer, stomach
CC   cancer, gallbladder cancer, renal cancer, prostatic cancer, breast
CC   cancer, esophageal cancer, hepatic cancer, oral cavity cancer, colon
CC   cancer, colorectal cancer, sarcoma, glioma and melanoma. The invention is
CC   also useful in gene therapy. The present sequence is human NK4 protein.
XX
SQ   Sequence 447 AA;

  Query Match             99.9%;  Score 2601;  DB 7;  Length 447;
  Best Local Similarity   99.8%;  Pred. No. 5.5e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 3
AAY98485
ID   AAY98485 standard; protein; 697 AA.
XX
AC   AAY98485;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Hepatocyte growth factor Pep 20 used in nucleic acid transporter system.
XX
KW   Transporter system; nucleic acid delivery; gene therapy; cancer;
KW   carcinogenesis; cardiovascular disease; infection.
XX
OS   Synthetic.
XX
PN   US6033884-A.
XX
PD   07-MAR-2000.
XX
PF   14-DEC-1993;   93US-00167641.
XX
PR   20-MAR-1992;   92US-00855389.
PR   19-MAR-1993;   93WO-US002725.
```

```
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Gottchalk S,  Sparrow J,  Cristiano RJ,  Woo SLC,  Smith LC;
XX
DR   WPI; 2000-281993/24.
XX
PT   System for transporting nucleic acid into cells, useful e.g. in gene
PT   therapy and for generating transgenic animals, comprises binding agent
PT   linked to nucleic acid, surface ligand and lytic agent.
XX
PS   Disclosure; Fig 23A; 108pp; English.
XX
CC   The present invention relates to a transporter system for delivering
CC   nucleic acid to a cell. The system comprises a nucleic acid binding
CC   complex, consisting of a binding molecule bonded non-covalently to the
CC   nucleic acid, and covalently to a surface ligand, and a lytic agent. The
CC   binding molecule is spermine or a spermidine derivative. Nucleotide
CC   sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used
CC   in the construction of the transporter system of the invention. The
CC   transporter system is used in gene therapy, particularly to deliver
CC   nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for
CC   treating cardiovascular disease, cancer, and infection. The transporter
CC   systems are also used to create transgenic animals (as models for human
CC   carcinogenesis or disease or for drug testing). Other uses include
CC   transforming cells to produce proteins , or transfecting cells in vitro
CC   to study the function of the nucleic acid. The use of a surface ligand
CC   allows specific targeting of selected cells and tissues. The lytic agent
CC   provides for release of the nucleic acid into the cellular interior, from
CC   endosomes, without requiring endosomal or lysosomal degradation
XX
SQ   Sequence 697 AA;

  Query Match             99.9%;  Score 2601;  DB 3;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 8.7e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 4
AAY59030
ID   AAY59030 standard; peptide; 697 AA.
XX
AC   AAY59030;
XX
DT   07-MAR-2000  (first entry)
XX
DE   Sequence of a peptide ligand Pep20.
XX
KW   Nucleic acid transport system; NTS; cell surface receptor; cytosis;
KW   nuclear membrane; lysis moiety; transgenic animal; human disease;
KW   nucleic acid delivery; cancer.
XX
OS   Synthetic.
XX
PN   US5994109-A.
XX
PD   30-NOV-1999.
XX
PF   03-JUN-1995;   95US-00460890.
XX
PR   20-MAR-1992;   92US-00855389.
PR   19-MAR-1993;   93WO-US002725.
PR   14-DEC-1993;   93US-00167641.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Woo SLC,  Cristiano RJ,  Gottchalk S,  Sparrow J,  Smith LC;
XX
DR   WPI; 2000-038262/03.
XX
PT   Nucleic acid transport system, useful for creating transgenic animals for
PT   assessing human disease such as cancer in an animal model.
XX
PS   Disclosure; Fig 23A; 107pp; English.
XX
CC   The invention relates to a nucleic acid transport system (NTS) for
CC   delivering nucleic acid into a cell. The NTS contains but is not limited
CC   to 5 components: (a) the nucleic acid or a macromolecule to be delivered;
CC   (b) a moiety that recognizes and binds to a cell surface receptor or
CC   antigen or is capable of entering a cell through cytosis; (c) a nucleic
CC   acid or macromolecular molecule binding moiety; (d) a moiety that is
CC   capable of moving or initiating movement through a nuclear membrane; and/
CC   or (e) a lysis moiety that enables the transport of the entire complex
CC   from the cell surface directly into the cytoplasm of the cell. The NTS
CC   delivers nucleic acid into the cellular interior as well as the nucleus
CC   of specific cells. The NTS can be used to treat disorders by targeting
CC   specific nucleic acid accordingly. The NTS can also be used to create
CC   transgenic animals for assessing human disease, such as cancer, in an
CC   animal model. The NTS can be used in vitro with tissue culture cells
CC   which allows the role of various nucleic acids to be studied by targeting
CC   specific expression into specifically targeted tissue culture cells. The
CC   lysis agent within the NTS avoids the problem of endosomal/lysosomal
CC   degradation
XX
SQ   Sequence 697 AA;

  Query Match             99.9%;  Score 2601;  DB 3;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 8.7e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 5
AAB45838
ID   AAB45838 standard; protein; 697 AA.
XX
AC   AAB45838;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Nucleic acid transporter system peptide ligand SEQ ID NO 50.
XX
KW   Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme;
KW   growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene;
KW   tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
KW   bacterial antigen.
XX
OS   Unidentified.
XX
PN   US6150168-A.
XX
PD   21-NOV-2000.
XX
PF   05-JUN-1995;   95US-00460971.
XX
PR   20-MAR-1992;   92US-00855389.
PR   19-MAR-1993;   93WO-US002725.
PR   14-DEC-1993;   93US-00167641.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Gottchalk S,  Sparrow J,  Cristiano RJ,  Smith LC,  Woo SLC;
XX
DR   WPI; 2001-049093/06.
XX
PT   Nucleic acid transporter system for delivering nucleic acid into a cell,
PT   useful for delivering proteins and polypeptides to cells, including
PT   growth factors, enzymes, hormones, and tumor suppressors.
XX
PS   Claim 8; Col 115-118; 105pp; English.
XX
CC   This invention describes a novel system (I) for delivering a nucleic acid
CC   to a cell, comprising a binding complex comprising a ligand binding
CC   molecule noncovalently bound to a nucleic acid and covalently linked to a
CC   surface ligand, and a second binding complex comprising a second binding
CC   molecule noncovalently bound to a nucleic acid and covalently linked to a
CC   nuclear ligand. The complexes are simultaneously bound to the nucleic
CC   acid. The nucleic acid transporter system can also be used in a method
CC   for the in vivo targeting of the insertion of DNA into a cell. It can
CC   also be used in processes for producing transformed cell lines. The
CC   system can be used to deliver a variety or proteins and polypeptides,
CC   such as hormones, growth factors, enzymes, clotting factors,
CC   apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor
CC   suppressors, viral antigens, parasitic antigens, and bacterial antigens.
CC   The transporter system uses lysis agents to overcome the problems of
CC   endosomal/lysosomal degradation seen with prior art systems
XX
SQ   Sequence 697 AA;

  Query Match             99.9%;  Score 2601;  DB 4;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 8.7e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 6
AAU04275
ID   AAU04275 standard; peptide; 697 AA.
XX
AC   AAU04275;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Nuclear ligand Pep20 used in nucleic acid transporter system.
XX
KW   Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule;
KW   gene therapy; hepatocyte; muscle; bone forming cell.
XX
OS   Synthetic.
XX
PN   US6177554-B1.
XX
PD   23-JAN-2001.
XX
PF   05-JUN-1995;   95US-00462040.
XX
PR   20-MAR-1992;   92US-00855389.
PR   19-MAR-1993;   93WO-US002725.
PR   14-DEC-1993;   93US-00167641.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Woo SLC,  Smith LC,  Cristiano RJ,  Gottchalk S,  Sparrow J;
XX
DR   WPI; 2001-365933/38.
XX
PT   Nucleic acid transport system, useful for creating transgenic animals for
PT   assessing human disease such as cancer in an animal model.
```

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XX
PS   Disclosure; Fig 23A; 111pp; English.
XX
CC   The sequence represents the nuclear ligand, Pep20, used in a nucleic acid
CC   transporter system. The nucleic acid transporter system uses nucleic acid
CC   binding complexes containing surface ligands which are capable of binding
CC   to a cell surface receptor and entering the cell through cytosis. The
CC   compounds of the invention are either ligands, binding molecules (surface
CC   ligands), lysis agents, spacer molecules or their intermediates. The
CC   ligands, binding molecules, lysis agents and spacer molecules are used in
CC   nucleic acid transporter systems to deliver nucleic acid into specific
CC   cells e.g. in gene therapy to deliver nucleic acid into hepatocytes,
CC   muscle cells or bone forming cells
XX
SQ   Sequence 697 AA;

  Query Match             99.9%;  Score 2601;  DB 4;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 8.7e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 7
AAR25676
ID   AAR25676 standard; protein; 728 AA.
XX
AC   AAR25676;
XX
DT   20-JAN-1993  (first entry)
XX
DE   Recombinant human hepatocyte growth factor.
XX
KW   HGF; enhance growth; preparing transgenic animals; hepatic disease;
KW   clinical diagnostic reagent; drug.
XX
OS   Homo sapiens.
XX
PN   JP04183394-A.
XX
PD   30-JUN-1992.
XX
PF   19-NOV-1990;   90JP-00314548.
XX
PR   19-NOV-1990;   90JP-00314548.
XX
PA   (TOYM ) TOYOBO KK.
PA   (NAKA/) NAKAMURA T.
XX
DR   WPI; 1992-265591/32.
XX
PT   Recombinant human hepatocyte growth factor and DNA encoding it - useful
PT   for diagnosis and treatment of hepatic disease and transgenic animal
PT   prepn.
XX
PS   Disclosure; Page 11; 28pp; Japanese.
XX
CC   This sequence represents a recombinant human hepatocyte growth factor. It
CC   has physiological activity, and using it enhanced growth of hepatocytes
CC   is possible. It is useful as a clinical diagnostic reagent, or a drug for
CC   treating hepatic disease. See also AAR25676-92, AAQ26713-27
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 8
AAR20005
ID   AAR20005 standard; protein; 728 AA.
XX
AC   AAR20005;
XX
DT   24-MAR-1992  (first entry)
XX
DE   Human hepatocyte growth factor.
XX
KW   HGF; kidney regeneration; nephritis.
XX
OS   Homo sapiens.
XX
PN   EP462549-A.
```

```
XX
PD   27-DEC-1991.
XX
PF   18-JUN-1991;   91EP-00109923.
XX
PR   19-JUN-1990;   90JP-00158841.
XX
PA   (TOYM ) TOYO BOSEKI KK.
XX
PI   Nakamuro T;
XX
DR   WPI; 1992-000939/01.
DR   N-PSDB; AAQ20049.
XX
PT   Agent contg. hepatocyte growth factor and carrier - used for treating
PT   renal diseases and promoting nephrocyte growth and as diagnostic for
PT   renal diseases.
XX
PS   Disclosure; Fig 1; 15pp; English.
XX
CC   Human HGF comprises an alpha-chain of 440 amino acids and a beta-chain of
CC   234 amino acids. There are 4 kringle domains in the alpha-chain, similar
CC   to that of plasmin; the beta-chain has about 37 per cent homology with
CC   the beta-chain of plasmin having serine protease activity. Homology of
CC   the amino acid sequence of rat HGF and human HGF is 91.6 per cent in the
CC   alpha-chain and 88.9 per cent in the beta-chain. HGF has been found to be
CC   an agent for nephrocyte growth and is useful as a treatment for renal
CC   failure
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 9
AAR40862
ID   AAR40862 standard; protein; 728 AA.
XX
AC   AAR40862;
XX
DT   14-MAR-1994  (first entry)
XX
DE   Competative inhibitor of HGF.
XX
KW   HGF; hepatocyte growth factor; transformation; antagonist; liver disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .31
FT                   /label= sig_peptide
FT   Protein         32. .728
FT                   /label= mat_protein
FT   Misc-difference 494
FT                   /note= "site of possible mutation"
XX
PN   JP05208998-A.
XX
PD   20-AUG-1993.
XX
PF   25-DEC-1991;   91JP-00357040.
XX
PR   25-DEC-1991;   91JP-00357040.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
DR   WPI; 1993-297806/38.
DR   N-PSDB; AAQ47832.
XX
PT   New protein is competitive inhibitor of hepatocyte growth factor - used
PT   in animal model of liver disease.
XX
PS   Claim 7; Page 8-11; 20pp; Japanese.
XX
CC   The gene encodes an inhibitor of HGF, which has a molecular weight of ca.
CC   76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and -
CC   B fragments were prepared from human HGF cDNA. This was amplified by PCR
CC   to give a human NP-HGF DNA fragment that was transformed into E.coli.
CC   (see AAQ47833) for a related sequence
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 10
AAR40863
ID   AAR40863 standard; protein; 728 AA.
XX
AC   AAR40863;
XX
DT   14-MAR-1994  (first entry)
XX
DE   Competative inhibitor of HGF.
XX
KW   HGF; hepatocyte growth factor; transformation; antagonist; liver disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .31
FT                   /label= sig_peptide
FT   Protein         32. .728
FT                   /label= mat_protein
FT   Misc-difference 489
FT                   /note= "site of possible mutation"
FT   Misc-difference 491
FT                   /note= "site of possible mutation"
FT   Misc-difference 494
FT                   /note= "site of possible mutation"
XX
PN   JP05208998-A.
XX
PD   20-AUG-1993.
XX
PF   25-DEC-1991;   91JP-00357040.
XX
PR   25-DEC-1991;   91JP-00357040.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
DR   WPI; 1993-297806/38.
DR   N-PSDB; AAQ47833.
XX
PT   New protein is competitive inhibitor of hepatocyte growth factor - used
PT   in animal model of liver disease.
XX
PS   Claim 6; Page 11-14; 20pp; Japanese.
XX
CC   The gene encodes an inhibitor of HGF, which has a molecular weight of ca.
CC   76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and -
CC   B fragments were prepared from human HGF cDNA. This was amplified by PCR
CC   to give a human NP-HGF DNA fragment that was transformed into E.coli.
CC   (see AAQ47833) for a related sequence
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 11
AAR42062
ID   AAR42062 standard; protein; 728 AA.
XX
AC   AAR42062;
XX
DT   25-MAR-2003  (revised)
DT   15-NOV-1993  (first entry)
XX
DE   Vascular endothelial cell growth enhancer protein.
XX
KW   Enhance; growth; vascular endothelial cell; human; tumour; cell line;
KW   HUOCA-II; HUOCA-III; blood vessel; wounds; burns; decubitus;
KW   post-operative tissue damage; drug; cardiac angiopathy.
XX
OS   Homo sapiens.
XX
PN   EP550296-A2.
XX
PD   07-JUL-1993.
XX
PF   27-NOV-1992;   92EP-00403199.
XX
PR   28-NOV-1991;   91JP-00337999.
XX
PA   (TERU ) TERUMO CORP.
XX
PI   Sudo T,  Harada K,  Hirahara I,  Adachi M;
XX
DR   WPI; 1993-215669/27.
DR   N-PSDB; AAQ45702.
XX
PT   Vascular endothelial cell growth factor protein - used for promoting
PT   angiogenesis in the treatment of cardiac angiopathy, wounds, burn
PT   injuries, postoperative tissue damage etc.
XX
PS   Claim 6; Page 18-21; 44pp; English.
XX
CC   This sequence represents a single chain protein which selectively
CC   enhances the growth of vascular endothelial cells. This protein was
CC   produced by the human tumour cell line HUOCA-II or HUOCA-III. This
CC   protein enhances the formation of new blood vessels and may be used to
CC   enhance healing of wounds, burns injuries, decubitus or post-operative
CC   tissue damage. It may also be used as a drug for cardiac angiopathy.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
```

```
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 12
AAR87522
ID   AAR87522 standard; protein; 728 AA.
XX
AC   AAR87522;
XX
DT   21-JUN-1996  (first entry)
XX
DE   Mutant hepatocyte growth factor #1 with changes at residues 491-495.
XX
KW   Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;
KW   injury; blood vessel; point mutation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 491. .495
FT                   /note= "change from wild type sequence: Lys-Glu-Leu-Arg-
FT                   Val to Ile-Glu-Gly-Arg-Thr"
XX
PN   JP07304796-A.
XX
PD   21-NOV-1995.
XX
PF   07-MAY-1994;   94JP-00117506.
XX
PR   07-MAY-1994;   94JP-00117506.
XX
PA   (TERU ) TERUMO CORP.
XX
DR   WPI; 1996-035890/04.
XX
PT   Novel derivative of hepatocyte growth factor - comprises a mutation at
PT   positions 492-494, for use in treating injured blood vessels.
XX
PS   Disclosure; Page; 8pp; Japanese.
XX
CC   The amino acid of the hepatocyte growth factor (HGF) generated to contain
CC   amino acid changes at residues 492-494. (Note - this sequence is not
CC   given in the specification but is based on the HGF sequence given in
CC   AAR20005). The generated mutant contains the sequence Ile-Glu-Gly-Arg-
CC   Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF
CC   is translated as single chain protein which is activated to a two chain
CC   protein by protease cleavage between residues 494-5, producing the alpha
CC   and beta chains. The novel sequence alters the protease recognition site,
CC   putatively introducing a Factor Xa recognition site. The novel HGF deriv.
CC   can be activated specifically at the site of injury in a blood vessel.
CC   (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were
CC   generated by point mutations using the oligonucleotides AAT06762-5
XX
SQ   Sequence 728 AA;

  Query Match           99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 13
AAR87524
ID   AAR87524 standard; protein; 728 AA.
XX
AC   AAR87524;
XX
DT   21-JUN-1996  (first entry)
XX
DE   Mutant hepatocyte growth factor #3 with changes at residues 491-495.
XX
KW   Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;
KW   injury; blood vessel; point mutation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 491. .495
FT                   /note= "change from wild type sequence: Lys-Glu-Leu-Arg-
FT                   Val to Lys-Gln-Gly-Arg-Thr"
XX
PN   JP07304796-A.
XX
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PD   21-NOV-1995.
XX
PF   07-MAY-1994;   94JP-00117506.
XX
PR   07-MAY-1994;   94JP-00117506.
XX
PA   (TERU ) TERUMO CORP.
XX
DR   WPI; 1996-035890/04.
XX
PT   Novel derivative of hepatocyte growth factor - comprises a mutation at
PT   positions 492-494, for use in treating injured blood vessels.
XX
PS   Disclosure; Page; 8pp; Japanese.
XX
CC   The amino acid of the hepatocyte growth factor (HGF) generated to contain
CC   amino acid changes at residues 492-494. (Note - this sequence is not
CC   given in the specification but is based on the HGF sequence given in
CC   AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-
CC   Thr, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF
CC   is translated as single chain protein which is activated to a two chain
CC   protein by protease cleavage between residues 494-5, producing the alpha
CC   and beta chains. The novel sequence alters the protease recognition site,
CC   putatively introducing a Factor Xa recognition site. The novel HGF deriv.
CC   can be activated specifically at the site of injury in a blood vessel.
CC   (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were
CC   generated by point mutations using the oligonucleotides AAT06762-5
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 14
AAR87525
ID   AAR87525 standard; protein; 728 AA.
XX
AC   AAR87525;
XX
DT   21-JUN-1996  (first entry)
XX
DE   Mutant hepatocyte growth factor #4 with changes at residues 491-495.
XX
KW   Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;
KW   injury; blood vessel; point mutation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 491. .495
FT                   /note= "change from wild type sequence: Lys-Glu-Leu-Arg-
FT                   Val to Lys-Gln-Gly-Arg-Val"
XX
PN   JP07304796-A.
XX
PD   21-NOV-1995.
XX
PF   07-MAY-1994;   94JP-00117506.
XX
PR   07-MAY-1994;   94JP-00117506.
XX
PA   (TERU ) TERUMO CORP.
XX
DR   WPI; 1996-035890/04.
XX
PT   Novel derivative of hepatocyte growth factor - comprises a mutation at
PT   positions 492-494, for use in treating injured blood vessels.
XX
PS   Disclosure; Page; 8pp; Japanese.
XX
CC   The amino acid of the hepatocyte growth factor (HGF) generated to contain
CC   amino acid changes at residues 492-494. (Note - this sequence is not
CC   given in the specification but is based on the HGF sequence given in
CC   AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-
CC   Val, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF
CC   is translated as single chain protein which is activated to a two chain
CC   protein by protease cleavage between residues 494-5, producing the alpha
CC   and beta chains. The novel sequence alters the protease recognition site,
CC   putatively introducing a Factor Xa recognition site. The novel HGF deriv.
CC   can be activated specifically at the site of injury in a blood vessel.
CC   (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were
CC   generated by point mutations using the oligonucleotides AAT06762-5
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391
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Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 15
AAR87523
ID   AAR87523 standard; protein; 728 AA.
XX
AC   AAR87523;
XX
DT   21-JUN-1996  (first entry)
XX
DE   Mutant hepatocyte growth factor #2 with changes at residues 491-495.
XX
KW   Hepatocyte growth factor; protease; cleavage recognition site; Factor Xa;
KW   injury; blood vessel; point mutation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 491. .495
FT                   /note= "change from wild type sequence: Lys-Glu-Leu-Arg-
FT                   Val to Lys-Gln-Gly-Arg-Ile"
XX
PN   JP07304796-A.
XX
PD   21-NOV-1995.
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PR   07-MAY-1994;   94JP-00117506.
XX
PA   (TERU ) TERUMO CORP.
XX
DR   WPI; 1996-035890/04.
XX
PT   Novel derivative of hepatocyte growth factor - comprises a mutation at
PT   positions 492-494, for use in treating injured blood vessels.
XX
PS   Disclosure; Page; 8pp; Japanese.
XX
CC   The amino acid of the hepatocyte growth factor (HGF) generated to contain
CC   amino acid changes at residues 492-494. (Note - this sequence is not
CC   given in the specification but is based on the HGF sequence given in
CC   AAR20005). The generated mutant contains the sequence Lys-Gln-Gly-Arg-
CC   Ile, which replaces the wild type sequence Lys-Glu-Leu-Arg-Val. The HGF
CC   is translated as single chain protein which is activated to a two chain
CC   protein by protease cleavage between residues 494-5, producing the alpha
CC   and beta chains. The novel sequence alters the protease recognition site,
CC   putatively introducing a Factor Xa recognition site. The novel HGF deriv.
CC   can be activated specifically at the site of injury in a blood vessel.
CC   (See AAR87522-5 for different HGF derivs.). The novel HGF derivs. were
CC   generated by point mutations using the oligonucleotides AAT06762-5
XX
SQ   Sequence 728 AA;

  Query Match             99.9%;  Score 2601;  DB 2;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 9.1e-165;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


Search completed: October  3, 2005, 06:05:50
Job time : 174.465 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 06:06:02 ; Search time 242.355 Seconds
(without alignments)
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Title: US-09-674-377B-1
Perfect score: 2604
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2601	99.9	447	14	US-10-081-309-2	Sequence 2, Appli
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4	2601	99.9	726	17	US-10-872-198-120	Sequence 120, App
5	2601	99.9	726	20	US-11-021-951-120	Sequence 120, App
6	2601	99.9	728	8	US-08-605-221-2	Sequence 2, Appli
7	2601	99.9	728	16	US-10-813-805-10	Sequence 10, Appl
8	2601	99.9	728	16	US-10-475-616-2	Sequence 2, Appli
9	2601	99.9	728	17	US-10-498-332-7	Sequence 7, Appli
10	2565	98.5	727	16	US-10-149-103A-1	Sequence 1, Appli
11	2563.5	98.4	489	18	US-10-926-088A-2	Sequence 2, Appli
12	2563.5	98.4	723	8	US-08-605-221-4	Sequence 4, Appli
13	2563.5	98.4	1109	18	US-10-509-247A-20	Sequence 20, Appl
14	2541.5	97.6	723	13	US-10-133-912-18	Sequence 18, Appl
15	2539.5	97.5	723	13	US-10-133-912-19	Sequence 19, Appl
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25	1588	61.0	269	16	US-10-149-103A-2	Sequence 2, Appli
26	1471	56.5	290	14	US-10-283-769-8	Sequence 8, Appli
27	1180.5	45.3	670	15	US-10-210-130-152	Sequence 152, App
28	1180.5	45.3	706	18	US-10-450-763-49987	Sequence 49987, A
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36	1180.5	45.3	711	14	US-10-123-036-2	Sequence 2, Appli
37	1180.5	45.3	711	15	US-10-116-275-229	Sequence 229, App
38	1180.5	45.3	711	15	US-10-004-378A-118	Sequence 118, App
39	1180.5	45.3	711	15	US-10-004-378A-119	Sequence 119, App
40	1180.5	45.3	711	15	US-10-004-378A-120	Sequence 120, App
41	1180.5	45.3	711	15	US-10-096-625-132	Sequence 132, App
42	1180.5	45.3	711	15	US-10-096-625-133	Sequence 133, App
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44	1180.5	45.3	711	16	US-10-409-554-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-951-629-1
; Sequence 1, Application US/09951629
; Publication No. US20020004480A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Toshikazu
; TITLE OF INVENTION: Anti-Cancer Agent
; FILE REFERENCE: 4373-0101P
; CURRENT APPLICATION NUMBER: US/09/951,629
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: JP 300728
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: PCT/JP96/03105
; PRIOR FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: US 09/471,032
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-951-629-1

Query Match 99.9%; Score 2601; DB 9; Length 447;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

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Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 2
US-10-081-309-2
; Sequence 2, Application US/10081309
; Publication No. US20030012775A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffmann-La Roche Inc.
;  TITLE OF INVENTION: PEG Conjugates of NK4
;  FILE REFERENCE: 20859
;  CURRENT APPLICATION NUMBER: US/10/081,309
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: homosapiens
US-10-081-309-2

  Query Match             99.9%;  Score 2601;  DB 14;  Length 447;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 3
US-10-926-088A-1
; Sequence 1, Application US/10926088A
; Publication No. US20050164918A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA Toshikazu
;  APPLICANT:  MATSUMOTO Kunio
;  APPLICANT:  FUKUTA Kazuhiro
;  TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
;  FILE REFERENCE: 2004-1328A/WMC/01736
;  CURRENT APPLICATION NUMBER: US/10/926,088A
;  CURRENT FILING DATE:  2004-08-26
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
;   LENGTH: 494
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: alpha-chain of human hepatocyte growth factor
US-10-926-088A-1

  Query Match             99.9%;  Score 2601;  DB 18;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 4
US-10-872-198-120
; Sequence 120, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
;  APPLICANT: Ulrich HAUPTS
```

```
;  APPLICANT:  Andre KOLTERMANN
;  APPLICANT:  Andreas SCHEIDIG
;  APPLICANT:  Christian VOETSMEIER
;  APPLICANT:  Ulrich Kettling
;  TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
;  FILE REFERENCE: 04156.0002U4
;  CURRENT APPLICATION NUMBER: US/10/872,198
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 60/543,518
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/524,960
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: EP 04003058
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: EP 03025871
;  PRIOR FILING DATE: 2003-11-11
;  PRIOR APPLICATION NUMBER: EP 03025851
;  PRIOR FILING DATE: 2003-11-10
;  PRIOR APPLICATION NUMBER: EP 03013819
;  PRIOR FILING DATE: 2003-06-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
;   LENGTH: 726
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-872-198-120

  Query Match             99.9%;  Score 2601;  DB 17;  Length 726;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 89

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 269

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 329

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 389

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 449

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476


RESULT 5
US-11-021-951-120
; Sequence 120, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
;  APPLICANT: HAUPTS, Ulrich
;  APPLICANT:  KOLTERMANN, Andre
;  APPLICANT:  SCHEIDIG, Andreas
;  APPLICANT:  VOTSMEIER, Christian
;  APPLICANT:  Kettling, Ulrich
;  APPLICANT:  COCO, Wayne Michael
;  TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
;  TITLE OF INVENTION:  And Diagnostic Use Thereof
;  FILE REFERENCE: 04156.0002U5
;  CURRENT APPLICATION NUMBER: US/11/021,951
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: 10/872,198
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 60/543,518
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/524,960
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: EP 04003058
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: EP 03025871
;  PRIOR FILING DATE: 2003-11-11
;  PRIOR APPLICATION NUMBER: EP 03025851
;  PRIOR FILING DATE: 2003-11-10
;  PRIOR APPLICATION NUMBER: EP 03013819
;  PRIOR FILING DATE: 2003-06-18
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
;   LENGTH: 726
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-021-951-120

  Query Match             99.9%;  Score 2601;  DB 20;  Length 726;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 89

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 269

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 329

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 389

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 449

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476


RESULT 6
US-08-605-221-2
; Sequence 2, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
;  APPLICANT:  NAKAMURA, Toshikazu
```

```
;  TITLE OF INVENTION:  THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
;  FILE REFERENCE:  2520-0101P
;  CURRENT APPLICATION NUMBER: US/08/605,221
;  CURRENT FILING DATE:  1996-03-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2

  Query Match             99.9%;  Score 2601;  DB 8;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 7
US-10-813-805-10
; Sequence 10, Application US/10813805
; Publication No. US20040191902A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER  INC.
;  APPLICANT:  Hambor, John E.
;  APPLICANT:  Roach, Marsha L.
;  TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS
;  FILE REFERENCE: PC25028A
;  CURRENT APPLICATION NUMBER: US/10/813,805
;  CURRENT FILING DATE:  2004-03-30
;  PRIOR APPLICATION NUMBER: US 60/459,449
;  PRIOR FILING DATE: 2003-03-31
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-813-805-10

  Query Match             99.9%;  Score 2601;  DB 16;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 8
US-10-475-616-2
; Sequence 2, Application US/10475616
; Publication No. US20040236073A1
; GENERAL INFORMATION:
;  APPLICANT: Gherardi, Ermanno
;  APPLICANT:  Lietha, Daniel
;  APPLICANT:  Blundell, Thomas L
;  APPLICANT:  Chirgadze, Dimitry Y
;  TITLE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter
;  TITLE OF INVENTION:  Factor (HGF/SF) and Variants Thereof, and Their Use
;  FILE REFERENCE: 2502489-991180
;  CURRENT APPLICATION NUMBER: US/10/475,616
;  CURRENT FILING DATE:  2003-10-22
;  PRIOR APPLICATION NUMBER: PCT/GB02/01941
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: GB 0110430.6
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-475-616-2

  Query Match             99.9%;  Score 2601;  DB 16;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151
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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 9
US-10-498-332-7
; Sequence 7, Application US/10498332
; Publication No. US20050113284A1
; GENERAL INFORMATION:
;  APPLICANT: Nakamura, Motonao
;  APPLICANT:  Higuchi, Toshio
;  APPLICANT:  Yamasaki, Yoshiki
;  APPLICANT:  Orita, Takuya
;  TITLE OF INVENTION: PHARMACEUTICAL AGENTS AND METHODS FOR
;  TITLE OF INVENTION:  TISSUE AND VASCULAR REGENERATION
;  FILE REFERENCE: 14539-016US1
;  CURRENT APPLICATION NUMBER: US/10/498,332
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: PCT/JP02/13014
;  PRIOR FILING DATE: 2002-12-12
;  PRIOR APPLICATION NUMBER: JP 2002-352924
;  PRIOR FILING DATE: 2002-12-04
;  PRIOR APPLICATION NUMBER: JP 2001-380158
;  PRIOR FILING DATE: 2001-12-13
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-498-332-7

  Query Match             99.9%;  Score 2601;  DB 17;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2e-211;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 10
US-10-149-103A-1
; Sequence 1, Application US/10149103A
; Publication No. US20040121945A1
; GENERAL INFORMATION:
;  APPLICANT: Liang, Hong
;  APPLICANT:  Sim, Kim Lee
;  APPLICANT:  Day, Clara
;  TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
;  FILE REFERENCE: 05213-0592  43170-274540
;  CURRENT APPLICATION NUMBER: US/10/149,103A
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: PCT/US00/34039
;  PRIOR FILING DATE: 2000-12-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 727
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-149-103A-1

  Query Match             98.5%;  Score 2565;  DB 16;  Length 727;
  Best Local Similarity   98.2%;  Pred. No. 2.3e-208;
  Matches  438;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 RKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKA 61
              :|||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         33 KKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNNGLPFTCKAFVFDKA 92

Qy         62 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Qy        122 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 212

Qy        182 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 272

Qy        242 TLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQ 301
              |||||||||||||||||||:||||||:|||||||||||||| ||||||||||||||||||
Db        273 TLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGQGEGYRGTANTIWNGIPCQRWDSQ 332

Qy        302 YPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCY 361
              |||:|||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        333 YPHKHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSNGQDCY 392

Qy        362 RGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWC 421
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        393 RGNGKNYMGNLSQTRSGLTCSMWNKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWC 452

Qy        422 YTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        453 YTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 11
US-10-926-088A-2
; Sequence 2, Application US/10926088A
; Publication No. US20050164918A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA Toshikazu
;  APPLICANT:  MATSUMOTO Kunio
;  APPLICANT:  FUKUTA Kazuhiro
;  TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
;  FILE REFERENCE: 2004-1328A/WMC/01736
;  CURRENT APPLICATION NUMBER: US/10/926,088A
;  CURRENT FILING DATE:  2004-08-26
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: alpha-chain of human hepatocyte growth factor of five amino acid-
;   OTHER INFORMATION: type
US-10-926-088A-2

  Query Match            98.4%;  Score 2563.5;  DB 18;  Length 489;
  Best Local Similarity   98.7%;  Pred. No. 1.9e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              ||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 12
US-08-605-221-4
; Sequence 4, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
;  APPLICANT:  NAKAMURA, Toshikazu
;  TITLE OF INVENTION:  THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
;  FILE REFERENCE:  2520-0101P
;  CURRENT APPLICATION NUMBER: US/08/605,221
;  CURRENT FILING DATE:  1996-03-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: HGF-B (five amino acids deletion type)
US-08-605-221-4

  Query Match            98.4%;  Score 2563.5;  DB 8;  Length 723;
  Best Local Similarity   98.7%;  Pred. No. 3e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              ||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 13
US-10-509-247A-20
; Sequence 20, Application US/10509247A
; Publication No. US20050181064A1
; GENERAL INFORMATION:
;  APPLICANT: Japan Science and Technology Corporation
;  APPLICANT:  Kuroda, Shunichi
;  APPLICANT:  Tanizawa, Katsuyuki
;  APPLICANT:  Kondo, Akihiko
;  APPLICANT:  Ueda, Masakazu
;  APPLICANT:  Seno, Masaharu
;  APPLICANT:  Tada, Hiroko
;  TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING
;  TITLE OF INVENTION:  PROTEIN, FUSED WITH DISEASE-TREATING TARGET-CELL-SUBSTANCE
;  FILE REFERENCE: P023P01/US
;  CURRENT APPLICATION NUMBER: US/10/509,247A
;  CURRENT FILING DATE:  2004-09-28
;  PRIOR APPLICATION NUMBER: PCT/JP03/02602
;  PRIOR FILING DATE: 2003-03-05
;  PRIOR APPLICATION NUMBER: JP2002-97280
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
;   LENGTH: 1109
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-509-247A-20

  Query Match             98.4%;  Score 2563.5;  DB 18;  Length 1109;
  Best Local Similarity   98.7%;  Pred. No. 5e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 477

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 537

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        538 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 592

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 652

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 712

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 772

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 832

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        833 CYTGNPLIPWDYCPISRCEGDTTPTIV 859


RESULT 14
US-10-133-912-18
; Sequence 18, Application US/10133912
; Publication No. US20020165358A1
;   GENERAL INFORMATION:
;        APPLICANT: Kinosaki, Masahiko
;                   Yamaguchi, Kyoji
;                   Goto, Masaaki
;                   Murakami, Akihiko
;                   Ueda, Masatsugu
;                   Higashio, Kanji
;                   Yamashita, Yasushi
;        TITLE OF INVENTION: TCF MUTANT
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Burgess, Ryan and Wayne
;             STREET: 370 Lexington Avenue, Suite 2105
;             CITY: NEW YORK
;             STATE: NEW YORK
;             COUNTRY: UNITED STATES OF AMERICA
;             ZIP: 10017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3 1/5 inch diskette
;             COMPUTER: PC'S LIMITED SYSTEM 200
;             OPERATING SYSTEM: WORD FOR WINDOWS
;             SOFTWARE: MICROSOFT WINDOWS 98
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/133,912
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/700,519
;             FILING DATE: 26-Aug-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wayne, Milton J.
;             REGISTRATION NUMBER: 17,906
;             REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 212-683-8150
;             TELEFAX: 212-532-4285
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 723
;             TYPE: AMINO ACID
;             STRANDEDNESS: SINGLE
;             TOPOLOGY: LINEAR
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-133-912-18

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  Best Local Similarity   98.9%;  Pred. No. 2.2e-206;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    1;

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Db         37 NTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQC 96

Qy         66 LWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMI 125
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Db         97 LWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMI 156

Qy        126 PHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 185
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Qy        246 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 305
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Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        366 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 425
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RESULT 15
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; Sequence 19, Application US/10133912
; Publication No. US20020165358A1
;   GENERAL INFORMATION:
;        APPLICANT: Kinosaki, Masahiko
;                   Yamaguchi, Kyoji
;                   Goto, Masaaki
;                   Murakami, Akihiko
;                   Ueda, Masatsugu
;                   Higashio, Kanji
;                   Yamashita, Yasushi
;        TITLE OF INVENTION: TCF MUTANT
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Burgess, Ryan and Wayne
;             STREET: 370 Lexington Avenue, Suite 2105
;             CITY: NEW YORK
;             STATE: NEW YORK
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;             COUNTRY: UNITED STATES OF AMERICA
;             ZIP: 10017
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3 1/5 inch diskette
;             COMPUTER: PC'S LIMITED SYSTEM 200
;             OPERATING SYSTEM: WORD FOR WINDOWS
;             SOFTWARE: MICROSOFT WINDOWS 98
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/133,912
;             FILING DATE: 25-Apr-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/700,519
;             FILING DATE: 26-Aug-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wayne, Milton J.
;             REGISTRATION NUMBER: 17,906
;             REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 212-683-8150
;             TELEFAX: 212-532-4285
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 723
;             TYPE: AMINO ACID
;             STRANDEDNESS: SINGLE
;             TOPOLOGY: LINEAR
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-133-912-19

  Query Match             97.5%;  Score 2539.5;  DB 13;  Length 723;
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  Matches  437;  Conservative    1;  Mismatches    4;  Indels    5;  Gaps    1;

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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Job time : 243.355 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:32 ; Search time 1375.69 Seconds
(without alignments)
24.255 Million cell updates/sec

Title: US-09-674-377B-1
Perfect score: 2604
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2601	99.9	697	2	US-08-460-890A-50	Sequence 50, Appl
2	2601	99.9	697	3	US-08-167-641C-50	Sequence 50, Appl
3	2601	99.9	697	3	US-08-460-971A-50	Sequence 50, Appl
4	2601	99.9	697	3	US-08-462-040-50	Sequence 50, Appl
5	2601	99.9	728	1	US-07-815-333A-2	Sequence 2, Appli
6	2601	99.9	728	1	US-08-087-783A-22	Sequence 22, Appl
7	2601	99.9	728	4	US-08-605-221-2	Sequence 2, Appli
8	2563.5	98.4	487	4	US-09-601-040A-27	Sequence 27, Appl
9	2563.5	98.4	717	4	US-09-601-040A-6	Sequence 6, Appli
10	2563.5	98.4	717	4	US-09-601-040A-8	Sequence 8, Appli
11	2563.5	98.4	723	1	US-07-838-410-1	Sequence 1, Appli
12	2563.5	98.4	723	1	US-08-290-937B-1	Sequence 1, Appli
13	2563.5	98.4	723	1	US-08-290-937B-2	Sequence 2, Appli
14	2563.5	98.4	723	1	US-08-404-643-1	Sequence 1, Appli
15	2563.5	98.4	723	3	US-09-194-326-1	Sequence 1, Appli
16	2563.5	98.4	723	4	US-09-600-991-18	Sequence 18, Appl
17	2563.5	98.4	723	4	US-08-605-221-4	Sequence 4, Appli
18	2563.5	98.4	723	4	US-09-601-040A-10	Sequence 10, Appl
19	2563.5	98.4	729	4	US-09-601-040A-2	Sequence 2, Appli
20	2563.5	98.4	729	4	US-09-601-040A-4	Sequence 4, Appli
21	2560.5	98.3	723	3	US-08-030-410-3	Sequence 3, Appli
22	2557.5	98.2	723	1	US-08-290-937B-3	Sequence 3, Appli
23	2541.5	97.6	723	3	US-09-194-326-2	Sequence 2, Appli
24	2541.5	97.6	723	3	US-08-700-519J-18	Sequence 18, Appl
25	2539.5	97.5	723	3	US-09-194-326-3	Sequence 3, Appli
26	2539.5	97.5	723	3	US-08-700-519J-19	Sequence 19, Appl
27	1780.5	68.4	574	4	US-09-600-991-2	Sequence 2, Appli
28	1471	56.5	290	4	US-08-484-841A-8	Sequence 8, Appli
29	1447.5	55.6	563	4	US-09-600-991-4	Sequence 4, Appli
30	1180.5	45.3	711	1	US-08-184-012C-8	Sequence 8, Appli
31	1180.5	45.3	711	1	US-08-334-177-2	Sequence 2, Appli
32	1180.5	45.3	711	2	US-08-666-082B-1	Sequence 1, Appli
33	1180.5	45.3	711	2	US-08-766-982-2	Sequence 2, Appli
34	1180.5	45.3	711	3	US-09-296-219-2	Sequence 2, Appli
35	1180.5	45.3	711	4	US-09-600-991-20	Sequence 20, Appl
36	1180.5	45.3	711	4	US-09-601-040A-12	Sequence 12, Appl
37	1180.5	45.3	711	4	US-09-949-016-6981	Sequence 6981, Ap
38	1180.5	45.3	711	5	PCT-US95-13830-2	Sequence 2, Appli
39	1125	43.2	716	2	US-08-766-982-1	Sequence 1, Appli
40	1125	43.2	716	3	US-09-296-219-1	Sequence 1, Appli
41	1066	40.9	790	4	US-08-991-761A-13	Sequence 13, Appl
42	1059	40.7	812	1	US-08-248-629A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-08-460-890A-50
; Sequence 50, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,890A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 697 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-460-890A-50

  Query Match             99.9%;  Score 2601;  DB 2;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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RESULT 2
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; Sequence 50, Application US/08167641C
; Patent No. 6033884
;  GENERAL INFORMATION:
;    APPLICANT:  Woo, Savio L.C.
;    APPLICANT:  Smith, Louis C.
;    APPLICANT:  Cristiano, Richard J.
;    APPLICANT:  Gottchalk, Stephen
;    TITLE OF INVENTION:  NUCLEIC ACID TRANSPORTER SYSTEMS AND
;    TITLE OF INVENTION:  METHODS OF USE
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/167,641C
;      FILING DATE:  December 14, 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/855,389
;      FILING DATE:  March 20, 1992
;      APPLICATION NUMBER:  PCT/US93/02725
;      FILING DATE:  March 19, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  205/012
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  697 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-167-641C-50

  Query Match             99.9%;  Score 2601;  DB 3;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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RESULT 3
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; Sequence 50, Application US/08460971A
; Patent No. 6150168
;  GENERAL INFORMATION:
;    APPLICANT:  Woo, Savio L.C.
;    APPLICANT:  Smith, Louis C.
;    APPLICANT:  Cristiano, Richard J.
;    APPLICANT:  Gottchalk, Stephen
;    TITLE OF INVENTION:  NUCLEIC ACID TRANSPORTER SYSTEMS AND
;    TITLE OF INVENTION:  METHODS OF USE
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
```

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;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071-2066
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  FastSEQ for Windows 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/460,971A
;       FILING DATE:  June 5, 1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/167,641
;       FILING DATE:  December 14, 1993
;       APPLICATION NUMBER:  07/855,389
;       FILING DATE:  March 20, 1992
;       APPLICATION NUMBER:  PCT/US93/02725
;       FILING DATE:  March 19, 1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  212/063
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  697 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-460-971A-50

  Query Match             99.9%;  Score 2601;  DB 3;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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RESULT 4
US-08-462-040-50
; Sequence 50, Application US/08462040
; Patent No. 6177554
;  GENERAL INFORMATION:
;    APPLICANT:  Woo, Savio L.C.
;    APPLICANT:  Smith, Louis C.
;    APPLICANT:  Cristiano, Richard J.
;    APPLICANT:  Gottchalk, Stephen
;    TITLE OF INVENTION:  NUCLEIC ACID TRANSPORTER SYSTEMS AND
;    TITLE OF INVENTION:  METHODS OF USE
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,040
;      FILING DATE:  June 5, 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/167,641
;      FILING DATE:  December 14, 1993
;      APPLICATION NUMBER:  07/855,389
;      FILING DATE:  March 20, 1992
;      APPLICATION NUMBER:  PCT/US93/02725
;      FILING DATE:  March 19, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  212/078
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  697 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-462-040-50

  Query Match             99.9%;  Score 2601;  DB 3;  Length 697;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 5
US-07-815-333A-2
; Sequence 2, Application US/07815333A
; Patent No. 5342831
;  GENERAL INFORMATION:
;    APPLICANT:  Nakamura, Toshikazu
;    APPLICANT:  Matsumoto, Kunio
;    TITLE OF INVENTION:  EPITHELIOCYTE GROWTH ACCELERATOR
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/815,333A
;      FILING DATE:  19911227
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Robert F.
;      REGISTRATION NUMBER:  27555
;      REFERENCE/DOCKET NUMBER:  44069
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 616-5600
;      TELEFAX:  (312) 616-5700
;      TELEX:  25-3533
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  728 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-815-333A-2

  Query Match             99.9%;  Score 2601;  DB 1;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2.9e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 6
US-08-087-783A-22
; Sequence 22, Application US/08087783A
; Patent No. 5547856
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
;    TITLE OF INVENTION:  HEPATOCYTE GROWTH FACTOR VARIANTS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,783A
;      FILING DATE:  13-Jul-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/884811
;      FILING DATE:  18-MAY-92
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/885971
;      FILING DATE:  18-MAY-92
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P0755779P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5416
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  728 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-087-783A-22

  Query Match             99.9%;  Score 2601;  DB 1;  Length 728;
  Best Local Similarity   99.8%;  Pred. No. 2.9e-214;
  Matches  446;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 7
US-08-605-221-2
; Sequence 2, Application US/08605221
; Patent No. 6699837
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Toshikazu
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
; FILE REFERENCE: 2520-0101P
; CURRENT APPLICATION NUMBER: US/08/605,221
; CURRENT FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2

Query Match 99.9%; Score 2601; DB 4; Length 728;
Best Local Similarity 99.8%; Pred. No. 2.9e-214;
Matches 446; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 8
US-09-601-040A-27
; Sequence 27, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; FILE REFERENCE: 0471-0161P
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-040A-27

Query Match 98.4%; Score 2563.5; DB 4; Length 487;
Best Local Similarity 98.7%; Pred. No. 2.8e-211;
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||      ||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473
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RESULT 9

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US-09-601-040A-6
; Sequence 6, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 717
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-6

  Query Match             98.4%;  Score 2563.5;  DB 4;  Length 717;
  Best Local Similarity   98.7%;  Pred. No. 4.6e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 10
US-09-601-040A-8
; Sequence 8, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 717
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-8

  Query Match             98.4%;  Score 2563.5;  DB 4;  Length 717;
  Best Local Similarity   98.7%;  Pred. No. 4.6e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 11
US-07-838-410-1
; Sequence 1, Application US/07838410
; Patent No. 5328836
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  HIGASHIO, KANJI
;    APPLICANT:  NAGAO, MASAYA
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  TAKAOKA, HIROAKI
;    APPLICANT:  TSUDA, EISUKE
;    TITLE OF INVENTION:  PLASMIDS CONTAINING DNA ENCODING THE
;    TITLE OF INVENTION:  AMINO ACID SEQUENCE OF TCF-II, TRANSFORMED CELLS WITH THE
;    TITLE OF INVENTION:  PLASMIDS, AND PRODUCTION MEDTHOD OF BIOLOGICALLY ACTIVE
;    TITLE OF INVENTION:  SUBSTANCE USING THE TRANSFORMED CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD.
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/838,410
;      FILING DATE:  19920311
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  PCT/JP91/00942
;      FILING DATE:  15-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 185852-1990
;      FILING DATE:  13-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WHITE, JOHN L.
;      REGISTRATION NUMBER:  17,746
;      REFERENCE/DOCKET NUMBER:  WAK 110
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Fibroblast
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  393..405
;      OTHER INFORMATION:  /note= "INTERNAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE IN ALPHA-CHAIN"
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  490..505
;      OTHER INFORMATION:  /note= "N-TERMINAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE OF BETA-CHAIN"
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  605..623
;      OTHER INFORMATION:  /note= "INTERNAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE IN BETA-CHAIN"
US-07-838-410-1

  Query Match             98.4%;  Score 2563.5;  DB 1;  Length 723;
  Best Local Similarity   98.7%;  Pred. No. 4.7e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              ||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 12
US-08-290-937B-1
; Sequence 1, Application US/08290937B
; Patent No. 5648233
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, KYOJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  MURAKAMI, AKIHIKO
;    APPLICANT:  GOTO, MASAAKI
;    APPLICANT:  TSUDA, EISUKE
;    APPLICANT:  MASUNAGA, HIROAKI
;    APPLICANT:  TAKAHIRA, REIKO
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  UEDA, MASATSUGU
;    APPLICANT:  HIGASHIO, KANJI
;    TITLE OF INVENTION:  MODIFIED TCF
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,937B
;      FILING DATE:  19-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-290-937B-1

  Query Match             98.4%;  Score 2563.5;  DB 1;  Length 723;
  Best Local Similarity   98.7%;  Pred. No. 4.7e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266
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Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 13
US-08-290-937B-2
; Sequence 2, Application US/08290937B
; Patent No. 5648233
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, KYOJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  MURAKAMI, AKIHIKO
;    APPLICANT:  GOTO, MASAAKI
;    APPLICANT:  TSUDA, EISUKE
;    APPLICANT:  MASUNAGA, HIROAKI
;    APPLICANT:  TAKAHIRA, REIKO
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  UEDA, MASATSUGU
;    APPLICANT:  HIGASHIO, KANJI
;    TITLE OF INVENTION:  MODIFIED TCF
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,937B
;      FILING DATE:  19-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-290-937B-2

  Query Match             98.4%;  Score 2563.5;  DB 1;  Length 723;
  Best Local Similarity   98.7%;  Pred. No. 4.7e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 326

Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
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Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473


RESULT 14
US-08-404-643-1
; Sequence 1, Application US/08404643
; Patent No. 5658742
;  GENERAL INFORMATION:
;    APPLICANT:  HIGASHIO, KANJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  OOGAKI, FUMIKO
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, TESTA, HURWITZ &
;      ADDRESSEE:  THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/404,643
;      FILING DATE:  15-MAR-1995
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-034 (3999/35)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-404-643-1
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  Query Match           98.4%;  Score 2563.5;  DB 1;  Length 723;
  Best Local Similarity  98.7%;  Pred. No. 4.7e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

Qy        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240
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Db        207 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 266

Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
              |||||||||||||||||||||||||||
Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473
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RESULT 15
US-09-194-326-1
; Sequence 1, Application US/09194326
; Patent No. 6306827
; GENERAL INFORMATION:
; APPLICANT: Kinosaki, Masahiko
; APPLICANT: Ogawa, Hiromi
; APPLICANT: Masanuga, Hiroaki
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Yamaguchi, Kyoji
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
; FILE REFERENCE: FJN-069
; CURRENT APPLICATION NUMBER: US/09/194,326
; CURRENT FILING DATE: 1998-11-24
; EARLIER APPLICATION NUMBER: PCT/JP98/01221
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: JP 94989
; EARLIER FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TCF-II
US-09-194-326-1

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  Query Match           98.4%;  Score 2563.5;  DB 3;  Length 723;
  Best Local Similarity  98.7%;  Pred. No. 4.7e-211;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180
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Db        152 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 206

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Qy        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300
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Qy        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360
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Db        327 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 386

Qy        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 446

Qy        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447
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Db        447 CYTGNPLIPWDYCPISRCEGDTTPTIV 473
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Search completed: October 3, 2005, 06:53:48
Job time : 1375.69 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 39.775 Seconds
(without alignments)
1069.209 Million cell updates/sec

Title: US-09-674-377B-2
Perfect score: 2579
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2563.5	99.4	728	1	JH0579	hepatocyte growth
2	2370.5	91.9	728	1	A60185	hepatocyte growth
3	2363.5	91.6	728	1	A35644	hepatocyte growth
4	1830	71.0	710	1	I51283	hepatocyte growth
5	1750	67.9	411	2	I51285	hepatocyte growth
6	1171	45.4	711	1	A47136	macrophage-stimula
7	1133.5	44.0	716	1	JC5061	macrophage-stimula
8	1114.5	43.2	716	1	A40332	macrophage-stimula
9	1054.5	40.9	790	1	PLPG	plasmin (EC 3.4.21
10	1039.5	40.3	812	1	PLMS	plasmin (EC 3.4.21
11	1036	40.2	810	2	I46260	plasmin (EC 3.4.21
12	1021	39.6	810	2	B30848	plasmin (EC 3.4.21
13	1019.5	39.5	812	1	PLBO	plasmin (EC 3.4.21
14	1018.5	39.5	810	1	PLHU	plasmin (EC 3.4.21
15	927	35.9	2869	2	T18518	apolipoprotein(a)
16	864.5	33.5	4548	1	S00657	apoprotein(a) (EC
17	840	32.6	1420	2	A32869	apolipoprotein(a)
18	457	17.7	460	2	B61545	plasmin (EC 3.4.21
19	450.5	17.5	455	2	A61545	plasmin (EC 3.4.21
20	406	15.7	336	2	S33879	plasmin precursor
21	357.5	13.9	625	1	TBBO	thrombin (EC 3.4.2
22	353	13.7	169	2	A40522	plasmin (EC 3.4.21
23	352.5	13.7	618	2	A35827	thrombin (EC 3.4.2
24	350	13.6	622	1	TBHU	thrombin (EC 3.4.2
25	344	13.3	617	2	S10511	thrombin (EC 3.4.2
26	302.5	11.7	562	1	UKHUT	t-plasminogen acti
27	302	11.7	559	1	A35029	t-plasminogen acti
28	291	11.3	559	1	A29941	t-plasminogen acti
29	270	10.5	120	2	E61545	plasmin (EC 3.4.21
30	268	10.4	123	2	C61545	plasmin (EC 3.4.21
31	260.5	10.1	89	2	A60140	plasmin (EC 3.4.21
32	237.5	9.2	946	1	A47299	ror-related recept
33	236.5	9.2	943	2	B45082	neurotrophic recep
34	228.5	8.9	603	2	S28941	coagulation factor
35	225	8.7	291	2	I38098	t-plasminogen acti
36	213.5	8.3	937	2	A45082	neurotrophic recep
37	204	7.9	655	1	A46688	hepatocyte growth
38	200	7.8	615	1	KFHU12	coagulation factor
39	192.5	7.5	558	2	JC5878	plasma hyaluronan-
40	189	7.3	593	2	S45281	coagulation factor
41	186.5	7.2	560	1	JC4795	plasma hyaluronan-
42	182.5	7.1	806	2	T18840	hypothetical prote
43	158.5	6.1	433	1	JN0560	u-plasminogen acti
44	158.5	6.1	685	1	A48289	neurotrophic recep
45	158	6.1	442	1	UKPG	u-plasminogen acti

ALIGNMENTS

RESULT 1
JH0579
hepatocyte growth factor precursor [validated] - human
N;Alternate names: hepapoietin A; scatter factor
C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S06
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Title: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Accession: JH0579
A;Molecule type: DNA
A;Residues: 1-728 <SEK>
A;Cross-references: UNIPROT:P14210; DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333
A;Accession: JU0333
A;Molecule type: DNA
A;Residues: 1-481,'RT',484-728 <SE2>
R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth f
A;Reference number: A41140; MUID:91334393; PMID:1831266
A;Accession: A41140
A;Molecule type: mRNA
A;Residues: 1-728 <WEI>
A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, I
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth facto
A;Reference number: A36677; MUID:91025062; PMID:2145836
A;Accession: B36677
A;Molecule type: mRNA
A;Residues: 1-728 <SE3>
A;Cross-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032
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A;Residues: 1-161,167-728 <SE4>
A;Cross-references: EMBL:X16323
A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A;Reference number: A33512; MUID:89392017; PMID:2528952
A;Accession: A33512
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-728 <MIY>

A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A;Reference number: A39006; MUID:91110540; PMID:1824873
A;Accession: A39006
A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M55379
A;Experimental source: embryonic lung
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native and
A;Reference number: PH0114; MUID:91207365; PMID:1826837
A;Accession: PH0114
A;Molecule type: protein
A;Residues: 32-43;53-58 <YOS>
A;Experimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Accession: A37796
A;Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'X',5
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashi
Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676; PMID:2531289
A;Accession: S06794
A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,'
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
A;Experimental source: liver
A;Note: the authors translated the codon CAG for residue 727 as Glu
A;Note: part of this sequence, including the amino end of both the alpha and beta chains
R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
A;Reference number: I59214; MUID:93087571; PMID:1280830
A;Accession: I59214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-288,'ET' <HAR>
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor g
A;Reference number: S15443; MUID:91200041; PMID:1826653
A;Accession: S15443
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-288,'ET' <MIY2>
A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
A;Reference number: I52253; MUID:92062058; PMID:1835383
A;Accession: I52253
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 161-166 <SHI>
A;Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
C;Genetics:
A;Gene: GDB:HGF
A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homold

C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
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F;32-494/Domain: alpha chain #status experimental <ACH>
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F;211-288/Domain: kringle homology <KR2>
F;305-383/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR4>
F;495-728/Domain: beta chain #status experimental <BCH>
F;495-716/Domain: trypsin homology <TRY>
F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;487-604/Disulfide bonds: #status predicted

Query Match 99.4%; Score 2563.5; DB 1; Length 728;
Best Local Similarity 98.7%; Pred. No. 1.6e-175;
Matches 441; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
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Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
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Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
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Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 2
A60185
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; JU0231
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hep
A;Reference number: JC2117; MUID:94183257; PMID:8135822
A;Accession: JC2117
A;Molecule type: mRNA
A;Residues: 1-728 <SAS2>
A;Cross-references: UNIPROT:Q08048; GB:D10212; NID:g220435; PIDN:BAA01064.1; PID:g220436
A;Experimental source: fibroblast, COS-1 cell
A;Note: submitted to JIPID, May 1993
A;Accession: PC2064
A;Molecule type: protein
A;Residues: 496-504 <SA2>
R;Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

A;Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig
A;Reference number: A60185; MUID:90377927; PMID:2144630
A;Accession: A60185
A;Molecule type: protein
A;Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,'
R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 1993
A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A;Reference number: S43416; MUID:94060105; PMID:8241272
A;Accession: S43416
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <LIU>
A;Cross-references: EMBL:X72307
R;Liu, Y.
submitted to the EMBL Data Library, May 1993
A;Reference number: S45521
A;Accession: S45521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563,'H',565-728 <LI2>
A;Cross-references: EMBL:X72307
R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A;Title: Purification and characterization of biologically active scatter factor from ra
A;Reference number: S17173; MUID:91354223; PMID:1831975
A;Accession: S17173
A;Molecule type: protein
A;Residues: 496-517,'T',519 <COF>
R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A;Title: Hepatocytes and scatter factor.
A;Reference number: S10966; MUID:90326152; PMID:2142751
A;Accession: S10966
A;Status: preliminary
A;Molecule type: protein
A;Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Reference number: I48758; MUID:95122532; PMID:7822318
A;Accession: I48758
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-30 <RES>
A;Cross-references: EMBL:X81630; NID:g673451; PIDN:CAA57286.1; PID:g673452
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495,496-728/Product: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

Query Match 91.9%; Score 2370.5; DB 1; Length 728;
Best Local Similarity 89.9%; Pred. No. 9.9e-162;
Matches 402; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | |||||||||| : :|:||||:||||||||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              |||||||||||||:|||||||||||||||||||||||||||||:|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479
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RESULT 3
A35644
hepatocyte growth factor precursor - rat
N;Alternate names: hepapoietin A; scatter factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
C;Accession: A35644; S13211
R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamur
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of th
A;Reference number: A35644; MUID:90222197; PMID:2139229
A;Accession: A35644
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <TAS>
A;Cross-references: UNIPROT:P17945; GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133.1;
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
R;Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA du
A;Reference number: S13211; MUID:91031482; PMID:2146117
A;Accession: S13211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495/Product: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

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  Query Match             91.6%;  Score 2363.5;  DB 1;  Length 728;
  Best Local Similarity   89.3%;  Pred. No. 3.1e-161;
  Matches  399;  Conservative   23;  Mismatches   20;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||| | || :||||||||:||:||||| |||| ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLVKIKTKKVNSADECANRCIRNKGFPFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     |||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | ||||||| || : :|:||||:||||||:||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKMCAHSAVNETDVPMETTECIKGQGEGYRGTTNTIWNGIPCQRWDS 332

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              |||||||||||||:|||||||||||||||||||||||||||| :|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLTKNYCRNPDDDAHGPW 452

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||:||||||||||||||||||
Db        453 CYTGNPLVPWDYCPISRCEGDTTPTIV 479
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RESULT 4
I51283
hepatocyte growth factor precursor - clawed frog
N;Alternate names: hepapoietin A; scatter factor
C;Species: Xenopus sp. (clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-May-2004
C;Accession: I51283
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Mech. Dev. 49, 123-131, 1995
A;Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ear
A;Reference number: I51283; MUID:95267690; PMID:7748783
A;Accession: I51283
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-710 <NAK>
A;Cross-references: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933
A;Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F;42-477,478-709/Product: hepatocyte growth factor #status predicted <MAT>
F;42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;115-193/Domain: kringle homology <KR1>
F;198-275/Domain: kringle homology <KR2>
F;289-367/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR4>
F;478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;478-700/Domain: trypsin homology <TRY>
F;52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
F;470-588/Disulfide bonds: #status predicted

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  Query Match             71.0%;  Score 1830;  DB 1;  Length 710;
  Best Local Similarity   68.4%;  Pred. No. 3.8e-123;
  Matches  301;  Conservative   63;  Mismatches   68;  Indels    8;  Gaps    2;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |:||   ::||:|:||| ::: ||::|||  || : || ||:||||||||||| |||
Db         21 KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI 80

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| || ||:||:|:| ::   ||||| |||||:|| ||| :|:|| ::|| |: ||||:
Db         81 KRCHWFSFNTMSAGIKDKYDISFDLYEKKDYIRDCIHGKGSNYRGTRNVTKRGLACQPWN 140

Qy        123 SMIPHEHS-----YRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 177
              ||||||||     ||||||:|||||||:|||||||||| :||||::||||| ||||:|:|
Db        141 SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT 200

Qy        178 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 237
              |||| ||| ||:||||| ||||| | ||:||| |||||:|| :|||||||||: ||||||
Db        201 CNGEHYRGPMDYTESGKECQRWDLQRPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT 260

Qy        238 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 297
              ||| | ||:|||| |  : :|:||:   | :|::|||||||:|:| :||| |||||||:
Db        261 LDPDTSWEFCAIKPCVHSIVNNTDI---TKDCMKGQGEGYRGSVSTTYNGIQCQRWDSQF 317

Qy        298 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 357
              || |: ||||:|||| |||||||||||||||||||:|:|||| |  |: |:||
Db        318 PHLHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY 377

Qy        358 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY 417
              ||| | | ||:||  | ||||:||::|| || | ||| | | :|||||||:||||||||
Db        378 GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY 437

Qy        418 TGNPLIPWDYCPISRCEGDT 437
              | :| :|||||||||||||
Db        438 TDDPFVPWDYCPISRCEGDT 457
```

RESULT 5
I51285
hepatocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51285
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
A;Reference number: I51285; MUID:95237013; PMID:7720585
A;Accession: I51285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-411 <STR>
A;Cross-references: UNIPROT:Q90978; GB:S77480; NID:g998675; PID:g998676
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
F;124-197/Domain: kringle homology <KRG>
F;202-279/Domain: kringle homology <KR2>
F;296-374/Domain: kringle homology <KR3>

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  Query Match             67.9%;  Score 1750;  DB 2;  Length 411;
  Best Local Similarity   75.9%;  Pred. No. 1.1e-117;
  Matches  289;  Conservative   47;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:||||| |||||| :|:
Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:||||||||  ||||:|||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGES 182
              |||||||||||||:|||||||||||||||||::|:|:|||||| ||||||||||||
Db        150 SMIPHEHSYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMTCNGES 209

Qy        183 YRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHT 242
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```
Db        210 YRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYTLDPNT 269

Qy        243 RWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHD 302

Db        270 PWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQFPHQHN 329

Qy        303 MTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKN 362

Db        330 ITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYRGNGKS 389

Qy        363 YMGNLSQTRSGLTCSMWDKNM 383

Db        390 YMGNLSKTRFGLTCSTWDKNM 410
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RESULT 6
A47136
macrophage-stimulating protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
C;Accession: A40331; B40331; A47136; A61395
R;Han, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A;Title: Characterization of the DNF15S2 locus on human chromosome 3: identification of
A;Reference number: A40331; MUID:92002016; PMID:1655021
A;Accession: A40331
A;Molecule type: DNA
A;Residues: 1-711 <HA1>
A;Cross-references: UNIPROT:P26927; GB:M74179
A;Accession: B40331
A;Molecule type: mRNA
A;Residues: 1-711 <HA2>
A;Cross-references: GB:M74178; NID:g183976; PIDN:AAA50165.1; PID:g183977
R;Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A;Title: Cloning, sequencing, and expression of human macrophage stimulating protein (MS
A;Reference number: A47136; MUID:93340141; PMID:8393443
A;Accession: A47136
A;Molecule type: mRNA
A;Residues: 1-12,'C',14-622,'F',624-711 <YOS>
A;Cross-references: GB:L11924; NID:g398037; PIDN:AAA59872.1; PID:g398038
A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence
R;Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
J. Exp. Med. 173, 1227-1234, 1991
A;Title: Macrophage stimulating protein: purification, partial amino acid sequence, and
A;Reference number: A61395; MUID:91217635; PMID:1827141
A;Accession: A61395
A;Molecule type: protein
A;Residues: 230-247;288-291,'E',293-295,'X',297-301,'X',303,'E',305,'EX',308-310;326-331
A;Experimental source: plasma
C;Genetics:
A;Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
A;Cross-references: GDB:128833; OMIM:142408
A;Map position: 3p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-483,484-711/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;19-483/Domain: alpha chain #status predicted <ACH>
F;110-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR3>
F;370-448/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status predicted <BCH>
F;484-704/Domain: trypsin homology <TRY>
F;56-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,37
F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.4%; Score 1171; DB 1; Length 711;
Best Local Similarity 47.3%; Pred. No. 4.4e-76;
Matches 196; Conservative 60; Mismatches 148; Indels 10; Gaps 4;

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Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92

Db         50 VADAEECAGRC----GPLMDCRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG 149

Db        106 YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNPDGDPG 165

Qy        150 GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF 209

Db        166 GPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPF 225

Qy        210 LPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTEC 269

Db        226 EPGKFLDQGLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTVSC 283

Qy        270 IQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWC 329

Db        284 FRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAPWC 343

Qy        330 FTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHR 388

Db        344 FTLRPGMRAAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQCQRWSAETPHKPQ 403

Qy        389 HIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV 442

Db        404 FTFTSEPHAQLEENFCRNPDGDSHGPWCYTMDPRTPFDYCALRRCADDQPPSIL 457
```

RESULT 7
JC5061
macrophage-stimulating protein 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5061
R;Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, N
Biochem. Biophys. Res. Commun. 227, 273-280, 1996
A;Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in
A;Reference number: JC5061; MUID:97011126; PMID:8858136
A;Accession: JC5061
A;Molecule type: mRNA
A;Residues: 1-716 <OHS>
A;Cross-references: UNIPROT:P70521; EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g166
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>
F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
F;110-186/Domain: kringle homology <KRI1>
F;191-268/Domain: kringle homology <KRI2>
F;292-370/Domain: kringle homology <KRI3>
F;379-457/Domain: kringle homology <KRI4>
F;489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.0%; Score 1133.5; DB 1; Length 716;
Best Local Similarity 46.1%; Pred. No. 2.1e-73;
Matches 195; Conservative 68; Mismatches 141; Indels 19; Gaps 6;

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Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92

Db         50 VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLRAQLHHSSLCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG 149

Db        106 YVRTCIMDNGASYRGTVARTADGLPCQAWSRRFPNDHKYTPTPKNGLEENFCRNPDGDPR 165

Qy        150 GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF 209

Db        166 GPWCYTTNRSVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSHPF 225
```

```
Qy        210 LPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-------TMNDTDV 262
              ||::|||   |||||||||   |||||| ||:   |:| : :|  |        : :
Db        226 HPEKFPDKALKDNYCRNPDASERPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQQRN 285

Qy        263 PLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPD 322
              :: : | :|:|| |||| ||   |:||||||:| ||:|   || : |||||||:|||||
Db        286 KVKASNCFRGKGEDYRGTTNTTSAGVPCQRWDAQNPHQHRFVPEKYACKDLRENFCRNPD 345

Qy        323 GSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDK 381
              |||:|||||: | :|| :| ||| | :    : || |:|: | |::|:|| |: |  |
Db        346 GSEAPWCFTSRPGLRVAFCYQIPRCTEEVVPEGCYHGSGEQYRGSVSKTRKGVQCQHW-- 403

Qy        382 NMEDLHRHIFWEPDA--SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 439
              : |  |:  |    |  : |  |:||||| |:|||||| :|   :||| : ||: |  |
Db        404 SSETPHKPQFTPTSAPHAGLEANFCRNPDGDSHGPWCYTLDPETLFDYCALKRCDDDQPP 463

Qy        440 TIV 442
              :|:
Db        464 SIL 466
```

RESULT 8
A40332
macrophage-stimulating protein 1 precursor - mouse
N;Alternate names: hepatocyte growth factor-like protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A40332; B40332
R;Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991
A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
A;Reference number: A40332; MUID:92002017; PMID:1832957
A;Accession: A40332
A;Molecule type: DNA
A;Residues: 1-716 <DEG>
A;Cross-references: UNIPROT:P26928; GB:M74180; NID:g193831; PIDN:AAA50166.1; PID:g193832
A;Accession: B40332
A;Molecule type: mRNA
A;Residues: 1-18,'P',20-716 <DEG2>
A;Cross-references: GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
C;Genetics:
A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolo
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F;19-483/Domain: alpha chain #status experimental <ACH>
F;110-186/Domain: kringle homology <KR1>
F;191-268/Domain: kringle homology <KR2>
F;292-370/Domain: kringle homology <KR3>
F;379-457/Domain: kringle homology <KR4>
F;484-711/Domain: beta chain #status experimental <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match   43.2%; Score 1114.5; DB 1; Length 716;
  Best Local Similarity   45.9%; Pred. No. 4.8e-72;
  Matches 194; Conservative   67; Mismatches 143; Indels   19; Gaps   6;

```
Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
              |  |::|| ||    |    |:|| :: :   |   |:   |   :        |:: ||
Db         50 VADAEECARRC----GPLLDCRAFHYNMSSHGCQLLPWTQHSLHTQLYHSSLCHLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG 149
              |:| ||:  | ||:|||: |  |: || ||   |::| |       |:||:|||| |:
Db        106 YVRTCIMDNGVSYRGTVARTAGGLPCQAWSRRFPNDHKYTPTPKNGLEENFCRNPDGDPR 165

Qy        150 GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF 209
              ||||:|:|  ||:: | |  | |  |: |||| ||| :| ||||: ||||| | || | |
Db        166 GPWCYTTNRSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSHPF 225
```

```
Qy        210 LPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-------TMNDTDV 262
              ||:: ||   |||||||||  ||||||  ||:   |:| : :|  |        : :
Db        226 QPEKFLDKDLKDNYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQRRN 285

Qy        263 PLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPD 322
              :   | :|:|| |||| ||   |:||||||:| ||:|   || : |||||||:|||||
Db        286 KGKALNCFRGKGEDYRGTTNTTSAGVPCQRWDAQSPHQHRFVPEKYACKDLRENFCRNPD 345

Qy        323 GSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDK 381
              |||:|||||: | :|: :| ||| | :    : || |:|: | |::|:|| |: |  |
Db        346 GSEAPWCFTSRPGLRMAFCHQIPRCTEELVPEGCYHGSGEQYRGSVSKTRKGVQCQHW-- 403

Qy        382 NMEDLHRHIFWEPDASK--LNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTP 439
              : |  |:  |    | :  |  |:||||| |:||||||| :| | :||| : ||: |  |
Db        404 SSETPHKPQFTPTSAPQAGLEANFCRNPDGDSHGPWCYTLDPDILFDYCALQRCDDDQPP 463

Qy        440 TIV 442
              :|:
Db        464 SIL 466
```

RESULT 9
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A;Reference number: S03733
A;Accession: S03733
A;Molecule type: protein
A;Residues: 1-560 <SCH>
A;Cross-references: UNIPROT:P06867
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
A;Molecule type: protein
A;Residues: 1-57 <BRU>
R;Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F;1-790/Product: plasminogen #status predicted <PRO>
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted

```
  Query Match             40.9%;  Score 1054.5;  DB 1;  Length 790;
  Best Local Similarity   44.6%;  Pred. No. 1e-67;
  Matches  195;  Conservative   64;  Mismatches  133;  Indels   45;  Gaps   14;

Qy         25 ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 84
              :|  |      : ::|| :|       | |:|| :    :||:    || :| : :    :
Db         16 SLSRKQVAARSVEECAAKCEAETN--FICRAFQYHSKDQQCVVMAENSKTSPIARM--RD 71

Qy         85 FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRGK-----DLQEN 139
              |:| : |:  |  | |::|:|| | ||||: || ||   ||   |  :      |:||
Db         72 VVLFEKRIYLSECKTGNGKNYRGTTSKTKSGVICQKWSVSSPHIPKYSPEKFPLAGLEEN 131

Qy        140 YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 199
              |||||  :| ||||:|::|| |:: ||||:| | ||| |:|| | | :  | ||  || |
Db        132 YCRNPDNDEKGPWCYTTDPETRFDYCDIPEC-EDECMHCSGEHYEGKISKTMSGIECQSW 190

Qy        200 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMND 259
              |:|| | :|| ::|:|    |||||||:|||||:| ||: |||:| |   |    |
Db        191 GSQSPHAHGYLPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPNKRWEFCDIPRC--TTPPP 248

Qy        260 TDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 319
              |  |  | :|::|:|| |||||:   :|  |||| :| ||:|: ||||| ||:| |||||
Db        249 TSGP--TYQCLKGRGENYRGTVSVTASGHTCQRWSAQSPHKHNRTPENFPCKNLEENYCR 306

Qy        320 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMS-----H------------GQDCYRGNGKN 362
              ||||  :|||:|||  :|  || :||:|  |     |            ||||||::
Db        307 NPDGETAPWCYTTDSEVRWDYC-KIPSCGSSTTSTEHLDAPVPPEQTPVAQDCYRGNGES 365

Qy        363 YMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE------PDASKLNENYCRNPDDDAHGPWC 416
              |  |  | | :|  |  |       |||   |      |:|  |  |||||| |   |||
Db        366 YRGTSSTTITGRKCQSWVSMTP--HRH---EKTPGNFPNAG-LTMNYCRNPDAD-KSPWC 418

Qy        417 YTGNPLIPWDYCPISRC 433
              || :| : |:|| : :|
Db        419 YTTDPRVRWEYCNLKKC 435
```

RESULT 10
PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of t
A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514
A;Molecule type: mRNA
A;Residues: 1-812 <DEG>
A;Cross-references: UNIPROT:P20918; GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LI2>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin
mediately after dissociation from the clot. In the presence of the inhibitor, the activa
e inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. To
eful in treating solid tumors.
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-812/Product: plasminogen #status predicted <PRO>
F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <MAT>
F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3
 bonds: #status predicted
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

```
  Query Match             40.3%;  Score 1039.5;  DB 1;  Length 812;
  Best Local Similarity   43.1%;  Pred. No. 1.2e-66;
  Matches  190;  Conservative   64;  Mismatches  144;  Indels   43;  Gaps   13;

Qy         30 TKKVNTA---DQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||   |     |  :|       | |::| :    :||:    || :| : :    :
Db         37 TKKQLAAGGVSDCLAKCEGE--TDFVCRSFQYHSKEQQCVIMAENSKTSSIIRM--RDVI 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR-----GKDLQENYC 141
              |:| : |:  |  | |  |:||:| ||||: || | :  ||  :|       : |:||||
Db         93 LFEKRVYLSECKTGIGNGYRGTMSRTKSGVACQKWGATFPHVPNYSPSTHPNEGLEENYC 152

Qy        142 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 201
              |||  :| ||||:|::|: ||: |:||:| | ||| |:|| | | :  | ||  || ||
Db        153 RNPDNDEQGPWCYTTDPDKRYDYCNIPECEE-ECMYCSGEKYEGKISKTMSGLDCQAWDS 211

Qy        202 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
              |:|| | ::| ::| |    ||| ||||:|||||:| ||  |||||  |   |
Db        212 QSPHAHGYIPAKFPSKNLKMNYCHNPDGEPRPWCFTTDPTKRWEYCDIPRCT----TPPP 267

Qy        262 VPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNP 321
              |  | :|::|:|| |||||:   :|  ||||  | || |: |||||  ||:| |||||||
Db        268 PPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNP 327

Qy        322 DGSESPWCFTTDPNIRVGYCSQIPNCDMSHG----------------QDCYRGNGKNYM 364
              ||  :|||:|||  :|  || :||:|: |                  |:||: :|::|
Db        328 DGETAPWCYTTDSQLRWEYC-EIPSCESSASPDQSDSSVPPEEQTPVVQECYQSDGQSYR 386

Qy.       365 GNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTGNP 421
              |  | | :|  |  |       |||       |||  |  |||||||  |  |||||| :|
Db        387 GTSSTTITGKKCQSWAAMFP--HRHSKTPENFPDAG-LEMNYCRNPDGD-KGPWCYTTDP 442

Qy        422 LIPWDYCPISRCEGDTTPTIV 442
              : |:|| : ||  :|  ::|
Db        443 SVRWEYCNLKRC-SETGGSVV 462
```

RESULT 11
I46260
plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46260
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fon
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipopro
A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: I46260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

```
A;Residues: 1-810 <LAW>
A;Cross-references: UNIPROT:Q29485; EMBL:U33171; NID:g1046360; PID:g1046361
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;379-456/Domain: kringle homology <KR4>
F;482-561/Domain: kringle homology <KR5>
F;582-803/Domain: trypsin homology <TRY>

  Query Match             40.2%;  Score 1036;  DB 2;  Length 810;
  Best Local Similarity   43.8%;  Pred. No. 2.2e-66;
  Matches  192;  Conservative   64;  Mismatches  134;  Indels   48;  Gaps   14;

Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||    | : ::|| :|    |   | |::| :    :||:    || |: | :    :
Db         37 TKKQLSVGSTEECAVKC--EKETSFICRSFQYHSKEQQCVIMAENSKSTPVLRM--RDVI 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR-----GKDLQENYC 141
              |:| | |:  |  :| |: |:|||| ||:|: || ||:  ||:  :       : | :|||
Db         93 LFEKKMYLSECKVGNGKYYRGTVSKTKTGLTCQKWSAETPHKPRFSPDENPSEGLDQNYC 152

Qy        142 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 201
              |||  :  ||||:| :|||||| |:| || | ||| |:|::| | :  | ||  || ||
Db        153 RNPDNDPKGPWCYTMDPEVRYEYCEIIQC-EDECMHCSGQNYVGKISRTMSGLECQPWDS 211

Qy        202 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
              | || | |:| ::| |    ||||||||:|||||:|:| : ||||| |  |       |
Db        212 QIPHPHGFIPSKFPSKNLKMNYCRNPDGEPRPWCFTMDRNKRWEYCDIPRCT------TP 265

Qy        262 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 319
               |    | :|: | || |:| |    :|: ||||  | || || ||||: ||:| |||||
Db        266 PPPSGPTYQCLMGNGEHYQGNVAVTVSGLTCQRWGEQSPHRHDRTPENYPCKNLDENYCR 325

Qy        320 NPDGSESPWCFTTDPNIRVGYCSQIPNC-----DMSHG--------------QDCYRGNG 360
              ||||  :||||||: ::|  :| :||:|     :  |                |:||:|||
Db        326 NPDGEPAPWCFTTNSSVRWEFC-KIPDCVSSASETEHSDAPVIVPPEQTPVVQECYQGNG 384

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCY 417
              : | |  | | :|  |  |       |||       |||  |  |||||| |  |||||
Db        385 QTYRGTSSTTITGKKCQPWTSMRP--HRHSKTPENYPDAD-LTMNYCRNPDGD-KGPWCY 440

Qy        418 TGNPLIPWDYCPISRCEG 435
              | :| : |::| : :| |
Db        441 TTDPSVRWEFCNLKKCSG 458


RESULT 12
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: B32869
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-810 <TOM>
A;Cross-references: UNIPROT:P12545; GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-9/Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted

  Query Match             39.6%;  Score 1021;  DB 2;  Length 810;
  Best Local Similarity   42.2%;  Pred. No. 2.6e-65;
  Matches  186;  Conservative   72;  Mismatches  127;  Indels   56;  Gaps   13;

Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||     : ::|| :|    :   |||::| :    :||:    |  || | :    :
Db         37 TKKQLGAGSIEECAAKCEEEE--EFTCRSFQYHSKEQQCVIMAENRKSSIVFRM--RDVV 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR-----GKDLQENYC 141
              |:| | |:  |  | |::|:||:| |::|| || |||  ||  ::       : |:|||| .
Db         93 LFEKKVYLSECKTGNGKNYRGTMSKTRTGITCQKWSSTSPHRPTFSPATHPSEGLEENYC 152

Qy        142 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 201
              |||  :  ||||:|::|| |:: ||||:| | ||| |:||:| | :  | ||  || ||
Db        153 RNPDNDGQGPWCYTTDPEERFDYCDIPEC-EDECMHCSGENYDGKISKTMSGLECQAWDS 211

Qy        202 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261
              |:|| | ::| ::|:|    ||||||||:|||||:| ||: ||| | |  |       |
Db        212 QSPHAHGYIPSKFPNKNLKKNYCRNPDGEPRPWCFTTDPNKRWELCDIPRCT------TP 265

Qy        262 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 319
               |    | :|::| || ||| |    :|  |  | :| || |: ||||| ||:| |||||
Db        266 PPSSGPTYQCLKGTGENYRGDVAVTVSGHTCHGWSAQTPHTHNRTPENFPCKNLDENYCR 325

Qy        320 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH-----------------GQDCYRGNGKN 362
              |||| ::|||:||:  :|  || :||:|: |                   |:|| |:|::
Db        326 NPDGEKAPWCYTTNSQVRWEYC-KIPSCESSPVSTEPLDPTAPPELTPVVQECYHGDGQS 384

Qy        363 YMGNLSQTRSGLTCSMW--------DKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGP 414
              | |  | | :|  |  |        :|  |:      |:|  |  |||||| |  ||
Db        385 YRGTSSTTTTGKKCQSWSSMTPHWHEKTPENF-------PNAG-LTMNYCRNPDAD-KGP 435

Qy        415 WCYTGNPLIPWDYCPISRCEG 435
              ||:| :| : |:|| : :| |
Db        436 WCFTTDPSVRWEYCNLKKCSG 456


RESULT 13
PLBO
plasmin (EC 3.4.21.7) precursor - bovine
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: S45046; A25835; I45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BER>
A;Cross-references: UNIPROT:P06868; EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g4949
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm
A;Reference number: A25835; MUID:85203906; PMID:3846532
A;Accession: A25835
A;Molecule type: protein
A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Residues: 706-743,'R',745-812 <MAL>
A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
F;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasminogen #status experimental <PRO>
F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <MAT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;110-188/Domain: kringle homology <KR1>
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR5>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
 bonds: #status predicted
F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

  Query Match             39.5%;  Score 1019.5;  DB 1;  Length 812;
  Best Local Similarity   42.0%;  Pred. No. 3.3e-65;
  Matches  183;  Conservative   73;  Mismatches  137;  Indels   43;  Gaps   12;

Qy         25 ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 84
              :|  |     : : || :|   :   | |:|| :    :||:    || :: | :    :
Db          42 SLSRKNLAGRSVEDCAAKC--EEETDFVCRAFQYHSKEQQCVVMAENSKNTPVFRM--RD 97

Qy         85 FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYRGK-----DLQEN 139
                ||| : |:  |  | |::|:|| : ||||: || ||:  ||   :  :      |:||
Db         98 VILYEKRIYLLECKTGNGQTYRGTTAETKSGVTCQKWSATSPHVPKFSPEKFPLAGLEEN 157

Qy        140 YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 199
              |||||  :| ||||:|::|: ||: ||||:| | :|| |:||:| | :  | ||: || |
Db        158 YCRNPDNDENGPWCYTTDPDKRYDYCDIPEC-EDKCMHCSGENYEGKIAKTMSGRDCQAW 216

Qy        200 DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMND 259
              | |:|| | ::| ::|:|    ||||||||:|||||:| ||  |||:| |  |
Db        217 DSQSPHAHGYIPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPQKRWEFCDIPRCT------ 270

Qy        260 TDVPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENY 317
              |  |       :|::| |: | |||     :|  ||||  | ||:|: ||||| ||:| |||
Db        271 TPPPSSGPKYQCLKGTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENY 330

Qy        318 CRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH----------------GQDCYRGNG 360
              ||||:| ::|||:||:  :|  ||: ||:|: |                  |||| |||
Db        331 CRNPNGEKAPWCYTTNSEVRWEYCT-IPSCESSPLSTERMDVPVPPEQTPVPQDCYHGNG 389

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCY 417
              ::| |  | | :|  |  |      |||:      |:|  |  ||||||| |   ||||
Db        390 QSYRGTSSTTITGRKCQSWSSMTP--HRHLKTPENYPNAG-LTMNYCRNPDAD-KSPWCY 445

Qy        418 TGNPLIPWDYCPISRC 433
              | :| : |::| : :|
Db        446 TTDPRVRWEFCNLKKC 461


RESULT 14
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A0
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fib
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <PET>
A;Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; GB:J05286; GB:M3427
A;Experimental source: leukocyte; lung fibroblast
R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in l
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human p
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
R;Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R;Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
A;Molecule type: protein
A;Residues: 581-810 <WI1>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pl

A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
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A;Molecule type: protein
A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
A;Molecule type: protein
A;Residues: 483-507,'E',509-604 <WI3>
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A;Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A;Reference number: A92125; MUID:73149248; PMID:4694729
A;Contents: annotation; active site
R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A;Reference number: A92382; MUID:82213905; PMID:6919539
A;Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A;Reference number: A92458; MUID:85054794; PMID:6094526
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ
A;Reference number: A58811; MUID:97067211; PMID:8910613
A;Contents: annotation
R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (M
A;Reference number: A58812; MUID:9548733; PMID:9548733
A;Contents: annotation
R;Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51488; PDB:2PK4
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A;Reference number: A51911; PDB:1PKR
A;Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R;Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A;Reference number: A52408; PDB:1PMK
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65244; PDB:1CEA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65245; PDB:1CEB
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation

R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65803; PDB:1HPJ
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65804; PDB:1HPK
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminog
A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many ot
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU a
d PIR:FGHUGB).
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately af
rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Tc
ting solid tumors.
C;Genetics:
A;Gene: GDB:PLG
A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-810/Product: plasminogen #status experimental <PRO>
F;20-96/Domain: activation peptide #status experimental <APT>
F;79-466/Product: angiostatin #status experimental <AST>
F;97-580,581-810/Product: plasmin #status experimental <MAT>
F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 39.5%; Score 1018.5; DB 1; Length 810;
Best Local Similarity 43.1%; Pred. No. 3.9e-65;
Matches 191; Conservative 67; Mismatches 138; Indels 47; Gaps 14;

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Qy         30 TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD 86
              |||     : ::|| :|  ::   |||:|| :    :||:     |  || : :    :
Db         37 TKKQLGAGSIEECAAKCEEDE--EFTCRAFQYHSKEQQCVIMAENRKSSIIIRM--RDVV 92

Qy         87 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHE-----HSYRGKDLQENYC 141
              |:| | |:  |  | |::|:||:| ||:|| || |||  ||       ::  : |:||||
Db         93 LFEKKVYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYC 152

Qy        142 RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 201
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Db        153 RNPDNDPQGPWCYTTDPEKRYDYCDILECEE-ECMHCSGENYDGKISKTMSGLECQAWDS 211

Qy        202 QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 261

Db        212 QSPHAHGYIPSKFPNKNLKKNYCRNPDRELRPWCFTTDPNKRWELCDIPRCT------TP 265

Qy        262 VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 319

Db        266 PPSSGPTYQCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCR 325

Qy        320 NPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH----------------GQDCYRGNGKN 362

Db        326 NPDGKRAPWCHTTNSQVRWEYC-KIPSCDSSPVSTEQLAPTAPPELTPVVQDCYHGDGQS 384

Qy        363 YMGNLSQTRSGLTCSMWDKNMEDLHRHIFWE---PDASKLNENYCRNPDDDAHGPWCYTG 419

Db        385 YRGTSSTTTTGKKCQSWSSMTP--HRHQKTPENYPNAG-LTMNYCRNPDAD-KGPWCFTT 440

Qy        420 NPLIPWDYCPISRCEGDTTPTIV 442

Db        441 DPSVRWEYCNLKKCSG-TEASVV 462


RESULT 15
T18518
apolipoprotein(a) - western European hedgehog (fragment)
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18518
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: T18518
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2869 <LAW>
A;Cross-references: UNIPROT:Q28398; EMBL:U33170; NID:g1046358; PID:g1046359; PIDN:AAC485
A;Experimental source: liver
C;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con
ent apolipoprotein(a).

  Query Match             35.9%;  Score 927;  DB 2;  Length 2869;
  Best Local Similarity   45.4%;  Pred. No. 4.9e-58;
  Matches  172;  Conservative   50;  Mismatches  123;  Indels   34;  Gaps   11;

Qy         89 ENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHS-----YRGKDLQENYCRN 143

Db       2490 EPLDLVDQCLEGTGENYRGNMAVTASGHTCQRWREQSPHSHSRTPENYPTKNLVGNYCRN 2549

Qy        144 PRGEEGGPWCFTSNPEVRYEVCDIPQCSE----------VECMTCNGESYRGLMDHTES 192

Db       2550 PDGEV-APWCYTTNSAMRWEYCSIPACESPTPPTEHLVVPEQCLEGNGENYQGNMAITVS 2608

Qy        193 GKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC 252

Db       2609 GQPCQGWRKQTPHRHEYTPENYPSKNLFGNYCRNPDGEIAPWCYTTNSAVRWEYCSIPTC 2668

Qy        253 ADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKD 312

Db       2669 -ESSSPPTEPMIIPDQCLEGTGENYRGSVAVTVSGHTCQRWREQSPHSHSRTPENYPTKN 2727

Qy        313 LRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH-------GQD-CYRGNGKNYM 364

Db       2728 LFGNYCRNPDGEVAPWCYTTNSAVRWEYC-KIPSCNSSSSPTEPSTSQDQCLKGNGESYQ 2786

Qy        365 GNLSQTRSGLTCSMWDKNMEDLHRHIFWEPD---ASKLNENYCRNPDDDAHGPWCYTGNP 421

Db       2787 GNISVTVSGYTCQRWRE--QTPHRHA-RTPDNYPCKNLVGNYCRNPDGEV-APWCYTTNS 2842

Qy        422 LIPWDYCPISRCEGDTTPT 440

Db       2843 AVRWEYCSIPTCESPTPPT 2861


Search completed: October  3, 2005, 05:59:59
Job time : 39.775 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 64.6344 Seconds
(without alignments)
3501.834 Million cell updates/sec

Title: US-09-674-377B-2
Perfect score: 2579
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2563.5	99.4	728	1	HGF_HUMAN	P14210 homo sapien
2	2424.5	94.0	730	2	Q867B7	Q867b7 canis famil
3	2418.5	93.8	730	2	Q76BS1	Q76bs1 bos taurus
4	2414.5	93.6	728	2	Q9BH09	Q9bh09 felis silve
5	2371.5	92.0	728	2	Q8C9G5	Q8c9g5 mus musculu
6	2370.5	91.9	728	1	HGF_MOUSE	Q08048 mus musculu
7	2363.5	91.6	728	1	HGF_RAT	P17945 rattus norv
8	2014.5	78.1	726	2	Q90978	Q90978 gallus gall
9	1830	71.0	710	2	Q91402	Q91402 xenopus. he
10	1718	66.6	405	2	Q788Q2	Q788q2 gallus gall
11	1204.5	46.7	449	2	Q6GP14	Q6gp14 xenopus lae
12	1198.5	46.5	716	2	Q91691	Q91691 xenopus lae
13	1184	45.9	704	2	Q90865	Q90865 gallus gall
14	1171	45.4	711	1	HGFL_HUMAN	P26927 homo sapien
15	1163.5	45.1	717	2	P70006	P70006 xenopus lae
16	1156	44.8	709	2	Q7ZTN9	Q7ztn9 xenopus lae
17	1152.5	44.7	709	2	Q90ZN6	Q90zn6 brachydanio
18	1151	44.6	567	2	Q13208	Q13208 homo sapien
19	1133.5	44.0	716	2	P70521	P70521 rattus norv
20	1114.5	43.2	716	1	HGFL_MOUSE	P26928 mus musculu
21	1114.5	43.2	716	2	Q91XG8	Q91xg8 mus musculu
22	1073.5	41.6	818	2	Q6PBA6	Q6pba6 brachydanio
23	1066	41.3	812	1	PLMN_RAT	Q01177 rattus norv
24	1056	40.9	806	1	PLMN_MACEU	O18783 macropus eu
25	1054.5	40.9	790	1	PLMN_PIG	P06867 sus scrofa
26	1044.5	40.5	466	2	Q6TCI0	Q6tci0 mus musculu
27	1044.5	40.5	812	1	PLMN_MOUSE	P20918 mus musculu
28	1040	40.3	215	2	O42341	O42341 gallus gall
29	1036	40.2	810	1	PLMN_ERIEU	Q29485 erinaceus e
30	1021	39.6	810	1	PLMN_MACMU	P12545 macaca mula
31	1019.5	39.5	812	1	PLMN_BOVIN	P06868 bos taurus
32	1018.5	39.5	810	1	PLMN_HUMAN	P00747 homo sapien
33	1013	39.3	759	2	Q7TP84	Q7tp84 rattus norv
34	971.5	37.7	359	2	Q8WMR1	Q8wmr1 canis famil
35	958	37.1	648	2	Q9H1V4	Q9h1v4 homo sapien
36	927	35.9	2869	2	Q28398	Q28398 erinaceus e
37	864.5	33.5	4548	1	APOA_HUMAN	P08519 homo sapien
38	858.5	33.3	211	2	O55027	O55027 mus musculu
39	840	32.6	1420	1	APOA_MACMU	P14417 macaca mula
40	617	23.9	162	2	Q8C4E2	Q8c4e2 mus musculu
41	577.5	22.4	109	2	Q9N1B8	Q9n1b8 ovis aries
42	444.5	17.2	454	2	O46506	O46506 papio hamad
43	439	17.0	75	2	Q9BGN9	Q9bgn9 bos taurus
44	406	15.7	325	1	PLMN_PETMA	P33574 petromyzon
45	400	15.5	429	2	Q8AVB0	Q8avb0 brachydanio

ALIGNMENTS

RESULT 1
HGF_HUMAN
ID HGF_HUMAN STANDARD; PRT; 728 AA.
AC P14210; Q02935; Q13494; Q14519; Q8TCE2; Q9BYL9; Q9BYM0; Q9UDU6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoeitin A).
GN Name=HGF; Synonyms=HPTA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91340155; PubMed=1831432; DOI=10.1016/0378-1119(91)90080-U;
RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=89392017; PubMed=2528952;
RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
RA Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
RA Gohda E., Daikuhara Y., Kitamura N.;
RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT growth factor.";
RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Leukocyte;
RX MEDLINE=91025062; PubMed=2145836;
RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T., Asami O.,
RA Hagiya M., Nakamura T., Shimizu S.;
RT "Isolation and expression of cDNA for different forms of hepatocyte
RT growth factor from human leukocyte.";
RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 55-73 AND 495-520.
RC TISSUE=Liver;
RX MEDLINE=90066676; PubMed=2531289; DOI=10.1038/342440a0;
RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
RA Sugimura A., Tashiro K., Shimizu S.;
RT "Molecular cloning and expression of human hepatocyte growth factor.";
RL Nature 342:440-443(1989).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=91200041; PubMed=1826653;
RA Miyazawa K., Kitamura A., Naka D., Kitamura N.;
RT "An alternatively processed mRNA generated from human hepatocyte
RT growth factor gene.";

RL Eur. J. Biochem. 197:15-22(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 583-592.
RC TISSUE=Lung fibroblast;
RX PubMed=1824873;
RA Rubin J.S., Chan A.M.-L., Bottaro D.P., Burgess W.H., Taylor W.G.,
RA Cech A.C., Hirschfield D.W., Wong J., Miki T., Finch P.W.,
RA Aaronson S.A.;
RT "A broad-spectrum human lung fibroblast-derived mitogen is a variant
RT of hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:415-419(1991).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=91334393; PubMed=1831266;
RA Weidner K.M., Arakaki N., Hartmann G., Vandekerckhove J., Weingart S.,
RA Rieder H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
RA Birchmeier W.;
RT "Evidence for the identity of human scatter factor and human
RT hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX PubMed=1720571;
RA Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid M.,
RA Aaronson S.A.;
RT "Identification of a competitive HGF antagonist encoded by an
RT alternative transcript.";
RL Science 254:1382-1385(1991).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND MUTAGENESIS OF ARG-494.
RX MEDLINE=93087571; PubMed=1280830;
RA Hartmann G., Naldini L., Weidner K.M., Sachs M., Vigna E.,
RA Comoglio P.M., Birchmeier W.;
RT "A functional domain in the heavy chain of scatter factor/hepatocyte
RT growth factor binds the c-Met receptor and induces cell dissociation
RT but not mitogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11574-11578(1992).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RX MEDLINE=96278713; PubMed=8662798; DOI=10.1074/jbc.271.22.13110;
RA Cioce V., Csaky K.G., Chan A.M.-L., Bottaro D.P., Taylor W.G.,
RA Jensen R., Aaronson S.A., Rubin J.S.;
RT "Hepatocyte growth factor (HGF)/NK1 is a naturally occurring
RT HGF/scatter factor variant with partial agonist/antagonist activity.";
RL J. Biol. Chem. 271:13110-13115(1996).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LYS-304 AND TYR-330.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [13]
RP SEQUENCE FROM N.A. (ISOFORMS 5 AND 6).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [14]
RP SEQUENCE OF 1-208 AND 249-695 FROM N.A. (ISOFORM 1).
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RT human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176(1991).
RN [15]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=91207365; PubMed=1826837;
RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
RA Hishida T., Daikuhara Y.;
RT "Identification of the N-terminal residue of the heavy chain of both
RT native and recombinant human hepatocyte growth factor.";
RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
RN [16]
RP CARBOHYDRATE-LINKAGE SITE THR-476.
RX MEDLINE=93129192; PubMed=1482348;
RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
RA Nakamura T., Shimizu S.;
RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
RT on the alpha chain.";
RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
RN [17]
RP MUTAGENESIS.
RX MEDLINE=92331602; PubMed=1321034;
RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
RA Baker J.B., Godowski P.J.;
RT "Structure-function analysis of hepatocyte growth factor:
RT identification of variants that lack mitogenic activity yet retain
RT high affinity receptor binding.";
RL EMBO J. 11:2503-2510(1992).
RN [18]
RP STRUCTURE BY NMR OF 31-127.
RX MEDLINE=98154323; PubMed=9493272; DOI=10.1016/S0969-2126(98)00012-4;
RA Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
RA Rubin J.S., Bottaro D.P., Byrd R.A.;
RT "The solution structure of the N-terminal domain of hepatocyte growth
RT factor reveals a potential heparin-binding site.";
RL Structure 6:109-116(1998).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.

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RX   MEDLINE=99036858; PubMed=9817840; DOI=10.1016/S0969-2126(98)00138-5;
RA   Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;

  Query Match             99.4%;  Score 2563.5;  DB 1;  Length 728;
  Best Local Similarity   98.7%;  Pred. No. 2e-185;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 2
Q867B7
ID   Q867B7      PRELIMINARY;      PRT;   730 AA.
AC   Q867B7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=HGF;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Beagle;
RX   MEDLINE=22844761; PubMed=12963274; DOI=10.1016/S0165-2427(03)00118-1;
RA   Miyake M., Saze K., Yaguchi T., Wang J., Suzuta Y., Haga Y.,
RA   Takahashi S.Y., Yamamoto Y., Iwabuchi S.;
RT   "Canine hepatocyte growth factor: molecular cloning and
RT   characterization of the recombinant protein.";
RL   Vet. Immunol. Immunopathol. 95:135-143(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Liao A.T., Chien M.B., London C.A.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB090353; BAC57560.1; -.
DR   EMBL; AY543632; AAS48570.1; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.982; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   730 AA;  83398 MW;  4E83F9EA8BFF6DB1 CRC64;

  Query Match             94.0%;  Score 2424.5;  DB 2;  Length 730;
  Best Local Similarity   91.9%;  Pred. No. 6.5e-175;
  Matches  411;  Conservative   19;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||||| || |||||||:|||||||||| ||||||||||||||||
Db         32 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              |||:|||||||||:|||||||||||||||||||||||||||| ||||||||||||||||||
Db         92 ARKRCLWFPFNSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||||||||||||||||||||||||||||||||||||:|||||||
Db        212 MTCNGESYRGPMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | ||||||| || :||||||||:||||||||||||||:|||||:|||||||||
Db        272 YTLDPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGTINTIWNGVPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||||:|||||||||||||||||||| ||:| ||||||||||
Db        332 QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              |||||||||||||:||||||||:|||||||||||||||||||:|||||||||||||||||
Db        392 YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||| ||||||||||||
Db        452 CYTGNPLIPWDYCPIFRCEGDTTPTIV 478


RESULT 3
Q76BS1
ID   Q76BS1      PRELIMINARY;      PRT;   730 AA.
AC   Q76BS1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=hgf;
OS   Bos taurus (Bovine).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamaji D., Kimura K., Watanabe A., Makondo K., Saito M.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB110822; BAD02475.1; -.
DR   HSSP; P08519; 1KIV.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   730 AA;  83357 MW;  E39D653B0A85F49B CRC64;

  Query Match             93.8%;  Score 2418.5;  DB 2;  Length 730;
  Best Local Similarity   91.5%;  Pred. No. 1.8e-174;
  Matches  409;  Conservative   22;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:||||:||||||| || |||||||:|||||||||| ||||||||||||||||
Db         32 QKKRRNTLHEFKRSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              |||:||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         92 ARKRCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||:||||||||||||||||||||||||||||||||:|||||
Db        212 MTCNGESYRGPMDHTETGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | ||||||| || :||||||:|::|||||||||||||:||||||||||||||
Db        272 YTLDPDTPWEYCAIKMCAHSTMNDTDLPMQTTECIQGQGEGYRGTINTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:||||||||||||||||:||||||||||||||||| ||:| ||||
Db        332 QYPHQHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||:||:|||||||||||||||||||||||:|||:|||||||||||||||
Db        392 YRGNGKNYMGSLSKTRSGLTCSMWDKNMEDLHRHIFWEPDATKLNKNYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 4
Q9BH09
ID   Q9BH09      PRELIMINARY;      PRT;   728 AA.
AC   Q9BH09;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hepatocyte growth factor HGF.
GN   Name=HGF;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Kobayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K.,
RA   Tsujimoto H.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Miyake M., Yaguchi T., Saze K., Suzuta Y., Wang J., Okazaki M.,
RA   Haga Y., Yamamoto Y., Takahashi S., Iwabuchi S.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AB046610; BAB21499.1; -.
DR   EMBL; AB080187; BAC10545.1; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.982; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   728 AA;  83067 MW;  8D7F4A333D1E190A CRC64;

  Query Match             93.6%;  Score 2414.5;  DB 2;  Length 728;
  Best Local Similarity   91.5%;  Pred. No. 3.7e-174;
  Matches  409;  Conservative   21;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:||||||||||||| || |||||||:|||||||||| ||||||||||||||||
Db         30 QKKRRNTLHEFKKSAKTTLIKEDPLLKIKTKKMNTADQCANRCIRNKGLPFTCKAFVFDK 89

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              |||:|||||||:|||||||||||||||||||||||||||| ||||||||||||||||||
Db         90 ARKRCLWFPFNSMTSGVKKEFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
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                |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||||||||| |||||||||||||||||||||||||||||:|||||
Db        210 MTCNGESYRGPMDHTESGKICQRWDRQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 269

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | ||||||| || :||||||||:||||||||||||||||:|:||||:|||||||
Db        270 YTLDPDTPWEYCAIKMCAHSTMNDTDVPMETTECIQGQGEGYRGTINSIWNGVPCQRWDS 329

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||:|||||||:|||||||||||||||||||| ||:| ||||
Db        330 QYPHQHDITPENFKCKDLRENFCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 389

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              |||||||||||||:||||||||:|||||||||||||||||||:|||||||||||||||||
Db        390 YRGNGKNYMGNLSKTRSGLTCSMWEKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 449

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476


RESULT 5
Q8C9G5
ID   Q8C9G5      PRELIMINARY;      PRT;   728 AA.
AC   Q8C9G5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A630060C16 product:hepatocyte growth factor, full
DE   insert sequence.
GN   Name=Hgf;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; AK042121; BAC31175.1; -.
DR   HSSP; P14210; 1GMN.
DR   MGD; MGI:96079; Hgf.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   728 AA;  82990 MW;  8D5258DF3BCF3545 CRC64;

  Query Match             92.0%;  Score 2371.5;  DB 2;  Length 728;
  Best Local Similarity   89.9%;  Pred. No. 6.6e-171;
  Matches  402;  Conservative   21;  Mismatches   19;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| ||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
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Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
                ||||| | |||||||||| : :|:||||:|||||||||||||| ||||||||||||
Db        273 YTLDPDTTWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
                ||||:||:|||||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
                ||||||||||||:|||||||||||||||||||||||||||:|||||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
                ||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479


RESULT 6
HGF_MOUSE
ID   HGF_MOUSE      STANDARD;      PRT;   728 AA.
AC   Q08048; Q61662; Q64007;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor precursor (Scatter factor) (SF)
DE   (Hepatopoeitin A).
GN   Name=Hgf;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
RC   TISSUE=Mammary fibroblast;
RX   MEDLINE=94183257; PubMed=8135822;
RA   Sasaki M., Nishio M., Sasaki T., Enami J.;
RT   "Identification of mouse mammary fibroblast-derived mammary growth
RT   factor as hepatocyte growth factor.";
RL   Biochem. Biophys. Res. Commun. 199:772-779(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94363381; PubMed=8081873;
RA   Lee C.C., Kozak C.A., Yamada K.M.;
RT   "Structure, genetic mapping, and expression of the mouse Hgf/scatter
RT   factor gene.";
RL   Cell Adhes. Commun. 1:101-111(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94060105; PubMed=8241272; DOI=10.1016/0167-4781(93)90159-B;
RA   Liu Y., Michalopoulos G.K., Zarnegar R.;
RT   "Molecular cloning and characterization of cDNA encoding mouse
RT   hepatocyte growth factor.";
RL   Biochim. Biophys. Acta 1216:299-303(1993).
CC   -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC       hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC       growth factor for a broad spectrum of tissues and cell types. It
CC       has no detectable protease activity.
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC       disulfide bond.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=Q08048-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=Q08048-2; Sequence=VSP_005408;
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC       subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10212; BAA01064.1; -.
DR   EMBL; D10213; BAA01065.1; -.
DR   EMBL; S71816; AAB31855.1; -.
DR   EMBL; X72307; CAA51054.1; ALT_INIT.
DR   PIR; JC2117; A60185.
DR   HSSP; P14210; 1BHT.
DR   MEROPS; S01.982; -.
DR   MGD; MGI:96079; Hgf.
DR   GO; GO:0008283; P:cell proliferation; IDA.
DR   GO; GO:0000902; P:cellular morphogenesis; IDA.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Growth factor; Kringle; Pyrrolidone carboxylic acid; Repeat;
KW   Serine protease homolog; Signal.
FT   SIGNAL        1     32       By similarity.
FT   CHAIN        33    495       Hepatocyte growth factor alpha chain.
FT   CHAIN       496    728       Hepatocyte growth factor beta chain.
FT   MOD_RES      33     33       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DOMAIN       38    124       PAN.
FT   DOMAIN      129    207       Kringle 1.
FT   DOMAIN      212    289       Kringle 2.
FT   DOMAIN      306    384       Kringle 3.
FT   DOMAIN      392    470       Kringle 4.
FT   DOMAIN      496    728       Serine protease-like.
FT   DISULFID     71     97       By similarity.
FT   DISULFID     75     85       By similarity.
FT   DISULFID    488    607       Interchain (By similarity).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    403    403       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    569    569       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    656    656       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    163    167       Missing (in isoform Short).
FT                                /FTId=VSP_005408.
FT   CONFLICT    344    344       N -> K (in Ref. 2).
FT   CONFLICT    479    479       V -> L (in Ref. 2).
FT   CONFLICT    564    564       R -> H (in Ref. 3).
SQ   SEQUENCE   728 AA;  82944 MW;  A0381FC497534328 CRC64;

  Query Match             91.9%;  Score 2370.5;  DB 1;  Length 728;
  Best Local Similarity   89.9%;  Pred. No. 7.8e-171;
  Matches  402;  Conservative   21;  Mismatches   19;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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              ::|||||:|||||||||||| | || |||||||||:||:||||| ||:|  ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLLKIKTKKVNSADECANRCIRNRGFTFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | |||||||||| : :|:||||:|||||||||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKTCAHSAVNETDVPMETTECIQGQGEGYRGTSNTIWNGIPCQRWDS 332

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||||||:|||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||:|||||||||||||||||||||||||||:|||||||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNKNYCRNPDDDAHGPW 452

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        453 CYTGNPLIPWDYCPISRCEGDTTPTIV 479
```

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RESULT 7
HGF_RAT
ID   HGF_RAT        STANDARD;      PRT;   728 AA.
AC   P17945;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Hepatocyte growth factor precursor (Scatter factor) (SF)
DE   (Hepatopoeitin A).
GN   Name=Hgf;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=90222197; PubMed=2139229;
RA   Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
RA   Shimizu S., Nakamura T.;
RT   "Deduced primary structure of rat hepatocyte growth factor and
RT   expression of the mRNA in rat tissues.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=91031482; PubMed=2146117;
RA   Okajima A., Miyazawa K., Kitamura N.;
RT   "Primary structure of rat hepatocyte growth factor and induction of
RT   its mRNA during liver regeneration following hepatic injury.";
RL   Eur. J. Biochem. 193:375-381(1990).
CC   -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC       hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC       growth factor for a broad spectrum of tissues and cell types. It
CC       has no detectable protease activity.
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC       disulfide bond.
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC       subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90102; BAA14133.1; -.
DR   EMBL; X54400; CAA38266.1; -.
DR   PIR; A35644; A35644.
DR   HSSP; P14210; 1BHT.
DR   MEROPS; S01.978; -.
DR   RGD; 2794; Hgf.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Direct protein sequencing; Glycoprotein; Growth factor; Kringle;
KW   Pyrrolidone carboxylic acid; Repeat; Serine protease homolog; Signal.
FT   SIGNAL       1     32       By similarity.
FT   CHAIN       33    495       Hepatocyte growth factor alpha chain.
FT   CHAIN      496    728       Hepatocyte growth factor beta chain.
FT   MOD_RES      33     33       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DOMAIN       38    124       PAN.
FT   DOMAIN      129    207       Kringle 1.
FT   DOMAIN      212    289       Kringle 2.
FT   DOMAIN      306    384       Kringle 3.
FT   DOMAIN      392    470       Kringle 4.
FT   DOMAIN      496    728       Serine protease-like.
FT   DISULFID     71     97       By similarity.
FT   DISULFID     75     85       By similarity.
FT   DISULFID    488    607       Interchain (By similarity).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    403    403       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    569    569       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    656    656       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   728 AA;  82905 MW;  3E0BF1F96ADCEDFF CRC64;

  Query Match             91.6%;  Score 2363.5;  DB 1;  Length 728;
  Best Local Similarity   89.3%;  Pred. No. 2.6e-170;
  Matches  399;  Conservative   23;  Mismatches   20;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              ::|||||:|||||||||||| | || :|||||||:||:||||| |||| ||||||||||
Db         33 QKKRRNTLHEFKKSAKTTLTKEDPLVKIKTKKVNSADECANRCIRNKGFPFTCKAFVFDK 92

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              :||:| |:|||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db         93 SRKRCYWYPFNSMSSGVKKGFGHEFDLYENKDYIRNCIIGKGGSYKGTVSITKSGIKCQP 152

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |:|||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        153 WNSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 212
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Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              |||||||||| |||||||| ||||| ||||||||||||||||||||||||||||:|||||
Db        213 MTCNGESYRGPMDHTESGKTCQRWDQQTPHRHKFLPERYPDKGFDDNYCRNPDGKPRPWC 272

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||| | ||||||| || : :|:||||:||||||:||||||||| ||||||||||||||
Db        273 YTLDPDTPWEYCAIKMCAHSAVNETDVPMETTECIKGQGEGYRGTTNTIWNGIPCQRWDS 332

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||:||:|||||||||||||||||||:||||||||||||||||||| ||:| ||||
Db        333 QYPHKHDITPENFKCKDLRENYCRNPDGAESPWCFTTDPNIRVGYCSQIPKCDVSSGQDC 392

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              |||||||||||||:|||||||||||||||||||||||||||| :|||||||||||||||
Db        393 YRGNGKNYMGNLSKTRSGLTCSMWDKNMEDLHRHIFWEPDASKLTKNYCRNPDDDAHGPW 452

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||:||||||||||||||||||
Db        453 CYTGNPLVPWDYCPISRCEGDTTPTIV 479


RESULT 8
Q90978
ID   Q90978      PRELIMINARY;      PRT;   726 AA.
AC   Q90978; Q90866;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor /scatter factor.
GN   Name=HGF/SF;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96029010; PubMed=7554499;
RA   Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
RT   "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions
RT   during early chick development.";
RL   Dev. Genet. 17:90-101(1995).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; X84045; CAA58864.1; -.
DR   PIR; I51285; I51285.
DR   HSSP; P14210; 1GMN.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   726 AA;  82865 MW;  5BD06CFB5C40B003 CRC64;

  Query Match             78.1%;  Score 2014.5;  DB 2;  Length 726;
  Best Local Similarity   75.5%;  Pred. No. 6.5e-144;
  Matches  336;  Conservative   49;  Mismatches   53;  Indels    7;  Gaps    2;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:|||||| |||||| :|:

Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:|||||||  ||||:|||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 177
              |||||||     |||||||:||||||||||||||||::|::|:|:|||||| ||||||||
Db        150 SMIPHEHSFLPSSYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMT 209

Qy        178 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 237
              |||||||| |||||||| ||||| | ||:||| ||||||||||||||||||: ||||||
Db        210 CNGESYRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYT 269

Qy        238 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 297
              |||:| ||:||||||    :| |:   ||| ||||||||||||||||:|| |||||||:
Db        270 LDPNTPWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQF 329

Qy        298 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 357
              ||:|::|||||||||||||||||||||||||||||||:||||||| ||:|: |||||
Db        330 PHQHNITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYR 389

Qy        358 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRH--IFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||:|||||| || ||||| ||||:||| ||  || ||| ||| :|||||||| ||||
Db        390 GNGKSYMGNLSNTRIGLTCSTWDKNIEDLRRHIQIFREPDVSKLKKNYCRNPDDDFHGPW 449

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPT 440
              ||| :|||||||||||| ||||||
Db        450 CYTDDPLIPWDYCPISRCTGDTTPT 474


RESULT 9
Q91402
ID   Q91402      PRELIMINARY;      PRT;   710 AA.
AC   Q91402;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor.
GN   Name=HGF;
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tailbud;
RX   MEDLINE=95267690; PubMed=7748783; DOI=10.1016/0925-4773(94)00309-B;
RA   Nakamura H., Tashiro K., Nakamura T., Shiokawa K.;
RT   "Molecular cloning of Xenopus HGF cDNA and its expression studies in
RT   Xenopus early embryogenesis.";
RL   Mech. Dev. 49:123-131(1995).
CC   -!- SIMILARITY: Belongs to peptidase family S1.
DR   EMBL; S77422; AAB34354.2; -.
DR   HSSP; P14210; 1GMN.
DR   MEROPS; S01.976; -.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
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DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   710 AA;  81487 MW;  5FE6480BE31C27FC CRC64;

  Query Match             71.0%;  Score 1830;  DB 2;  Length 710;
  Best Local Similarity   68.4%;  Pred. No. 5.6e-130;
  Matches  301;  Conservative   63;  Mismatches   68;  Indels    8;  Gaps    2;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |:||   ::||:|:||| ::: ||::|||  || : || ||:||||||||||||| |||
Db         21 KKRNAFDDYKKTAETTLTRLNKALEVKTKMFNTTENCAKRCSRNKGLPFTCKAFAFDKNI 80

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| || ||:||:|:| ::   ||||| |||||:|| ||| :|:|| ::|| |: ||||:
Db         81 KRCHWFSFNTMSAGIKDKYDISFDLYEKKDYIRDCIHGKGSNYRGTRNVTKRGLACQPWN 140

Qy        123 SMIPHEHS-----YRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMT 177
              ||||||||     ||||||:|||||||:|||||||||| :||||::||||| ||||:|:|
Db        141 SMIPHEHSFLPSTYRGKDLKENYCRNPKGEEGGPWCFTKSPEVRHDVCDIPFCSEVDCVT 200

Qy        178 CNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYT 237
              |||| ||| ||:||||| ||||| | ||:||| |||||:|| :|||||||||: ||||||
Db        201 CNGEHYRGPMDYTESGKECQRWDLQRPHKHKFRPERYPNKGLNDNYCRNPDGKSRPWCYT 260

Qy        238 LDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQY 297
              ||| | ||:|||| |  : :|:||:    | :|::|||||||:|:| :||| |||||||:
Db        261 LDPDTSWEFCAIKPCVHSIVNNTDI---TKDCMKGQGEGYRGSVSTTYNGIQCQRWDSQF 317

Qy        298 PHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 357
              || |: ||||:||||| ||||||||||||||||||||:|:|||| | |: |:||
Db        318 PHLHNFTPENYKCKDLSENYCRNPDGSESPWCFTTDPNIRIGHCSQIKKCQASNQQECYY 377

Qy        358 GNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCY 417
              ||| | | ||:||  | ||||:||::|| || | ||| | | :|||||||:||||||||
Db        378 GNGSTYKGTLSRTRFRLPCSMWEKNLQDLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCY 437

Qy        418 TGNPLIPWDYCPISRCEGDT 437
              | :| :|||||||||||||
Db        438 TDDPFVPWDYCPISRCEGDT 457


RESULT 10
Q788Q2
ID   Q788Q2      PRELIMINARY;      PRT;   405 AA.
AC   Q788Q2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   HGF/SF protein precursor (Fragment).
GN   Name=HGF/SF;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=95237013; PubMed=7720585;
RA   Streit A., Stern C.D., Thery C., Ireland G.W., Aparicio S.,
RA   Sharpe M.J., Gherardi E.;
RT   "A role for HGF/SF in neural induction and its expression in Hensen's
RT   node during gastrulation.";
RL   Development 121:813-824(1995).
DR   EMBL; X80131; CAA56430.1; -.
DR   HSSP; P00747; 1KI0.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   ProDom; PD000395; Kringle; 3.
DR   SMART; SM00130; KR; 3.
DR   SMART; SM00473; PAN_AP; 1.
DR   PROSITE; PS00021; KRINGLE_1; 3.
DR   PROSITE; PS50070; KRINGLE_2; 3.
DR   PROSITE; PS50948; PAN; 1.
KW   Kringle; Signal.
FT   SIGNAL       1     25       Potential.
FT   NON_TER     405    405
SQ   SEQUENCE   405 AA;  46550 MW;  EB7BAD4EF220B449 CRC64;

  Query Match             66.6%;  Score 1718;  DB 2;  Length 405;
  Best Local Similarity   75.7%;  Pred. No. 8.9e-122;
  Matches  284;  Conservative   47;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          3 KRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKAR 62
              |||| :|::||: :  |||::  |::||| :|| :||| ||:||||| |||||| :|:
Db         30 KRRNPLHDYKKTGELMLIKVNKTLEVKTKLLNTTEQCAKRCSRNKGLSFTCKAFAYDRVT 89

Qy         63 KQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWS 122
              |:| |  |||:::||:|:  | |||:| |||:||||||||  ||||:|||||||:|| |:
Db         90 KRCHWLSFNSLTNGVRKKQDHAFDLFEKKDYVRNCIIGKGAEYKGTISITKSGIQCQAWN 149

Qy        123 SMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGES 182
              ||||||||||||||:|||||||||||||||||||::|::|:|||||| ||||||||||||
Db        150 SMIPHEHSYRGKDLRENYCRNPRGEEGGPWCFTTSPQMRHEVCDIPLCSEVECMTCNGES 209

Qy        183 YRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHT 242
              ||| |||||||| ||||| | ||:||| |||||||||||||||||||: |||||||:|
Db        210 YRGPMDHTESGKECQRWDLQRPHKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYTLDPNT 269

Qy        243 RWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHD 302
              ||:||||||    :| |:  ||| |||||||||||||||:|| |||||||:||:|:
Db        270 PWEFCAIKTCDVGILNSTEAVAETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQFPHQHN 329

Qy        303 MTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKN 362
              :|||||||||||||||||||||||||||||||:|||||| ||:|: |||||||||:
Db        330 ITPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRIGYCSQIPKCDVSNEQDCYRGNGKS 389

Qy        363 YMGNLSQTRSGLTCS 377
              ||||||:|| |||||
Db        390 YMGNLSKTRFGLTCS 404


RESULT 11
Q6GP14
ID   Q6GP14      PRELIMINARY;      PRT;   449 AA.
AC   Q6GP14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC397993 protein.
GN   Name=LOC397993;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073334; AAH73334.1; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
KW   Kringle.
SQ   SEQUENCE   449 AA;  52467 MW;  5C2CE4B708E13D0B CRC64;

  Query Match             46.7%;  Score 1204.5;  DB 2;  Length 449;
  Best Local Similarity   47.0%;  Pred. No. 6.7e-83;
  Matches  205;  Conservative   74;  Mismatches  144;  Indels   13;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: :::::::|    |: ::    :| :  :    || :|:        |::||::   :
Db         21 RSALNDYQRSKGLELVHMNNG-GVKQEIQSEIQVCAKQCSD----LLDCRSFVYNWKSQS 75

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
              |   |:   |: |  :   ::|||: |||||:|::| | :|:|||| ||||  || |
Db         76 CRLLPWTQNSANVLLQRNVQYDLYQKKDYIRDCVVGNGNTYRGTVSKTKSGRTCQRWRLK 135

Qy        125 IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181
               ||:| :      ||:|||||||  :  ||||:|::  :|:: | | :| :  |:|||||
Db        136 FPHDHKFSPIHWPDLEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE 195

Qy        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241
              ||| :| ||||| ||||| |||| | : ||:|||| |||||||||   |||||| ||:
Db        196 DYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTDPN 255

Qy        242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH 301
               |:| |  |    ::: ::   |: | : :|||||  ||  :|||||||||  |  |
Db        256 VEKEFCRITKCKKQRLSNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDSQTPQSH 312

Qy        302 DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNG 360
              || : || | ||||||||||:|||||| | :|: || ||  | |     ||| |||
Db        313 RFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHGNG 372

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              : | | :|:|| |: |  |::   ||   :  :|    | |||||||| |:|||||| :
Db        373 ELYSGRVSKTRKGIKCRRWEEKRNDLELSLD-QPYLVPLEENYCRNPDRDSHGPWCYTMD 431

Qy        421 PLIPWDYCPISRCEGD 436
              |  |:||| |  |||:
Db        432 PNTPFDYCAIKPCEGE 447


RESULT 12
Q91691
ID   Q91691      PRELIMINARY;      PRT;   716 AA.
AC   Q91691;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Growth factor Livertine.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ruiz i Altaba A., Thery C.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U57455; AAB52574.1; -.
DR   HSSP; P00746; 1FDP.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease.
SQ   SEQUENCE   716 AA;  81971 MW;  508376A0E4398798 CRC64;

  Query Match             46.5%;  Score 1198.5;  DB 2;  Length 716;
  Best Local Similarity   46.5%;  Pred. No. 3.2e-82;
  Matches  205;  Conservative   75;  Mismatches  148;  Indels   13;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: ::::::|    |: ::    :| :  :    || :|:        |::||::   :
Db         31 RSALNDYQRSKGLELVHMNNG-GVKQEIQSEIQVCAKQCSD----LLDCRSFVYNWKSQT 85

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
              |   |:   |: |  :   ::|||: |||||:|: | | :|:|||| ||||  || |
Db         86 CRLLPWTQNSANVLLQRNVQYDLYQKKDYIRDCVAGNGNTYRGTVSKTKSGRTCQRWRLK 145

Qy        125 IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181
               ||:| :      :|:|||||||  :  ||||:|::  :|:: | | :| :  |:|||||
Db        146 FPHDHKFSPIHWPELEENYCRNPDSDPEGPWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE 205

Qy        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241
              ||| :| ||||| ||||| |||| | : ||:|||| |||||||||   |||||| ||:
Db        206 DYRGSVDRTESGKECQRWDLQTPHAHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTDPN 265
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Qy        242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH 301
              |:| | |    ::: ::   |: | : :|||||  ||  :||||||||| |  |
Db        266 VEKEFCRITKCKKQRLSNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDSQTPQSH 322

Qy        302 DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNG 360
              || : || | ||||||||||:|||||| | :|: || ||  | |      ||| |||
Db        323 RFLPEKYPCKGLDENYCRNPDGSEAPWCFTTLPGMRMAYCFQIKRCKDDVLEPDCYHGNG 382

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              : | | :|:|| |: |  |::   ||   :  :|    | |||||||| |:||||||| :
Db        383 ELYSGRVSKTRKGIKCRRWEEKRNDLELSLD-QPYLVPLEENYCRNPDRDSHGPWCYTMD 441

Qy        421 PLIPWDYCPISRCEGDTTPTI 441
              |  |:||| |  |||:   |:
Db        442 PNTPFDYCAIKPCEGEKVLTL 462
```

RESULT 13
Q90865
ID Q90865 PRELIMINARY; PRT; 704 AA.
AC Q90865;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hepatocyte growth factor-like/macrophage stimulating protein.
GN Name=HGF1/MSP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96029010; PubMed=7554499;
RA Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
RT "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions
RT during early chick development.";
RL Dev. Genet. 17:90-101(1995).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; X84043; CAA58862.1; -.
DR HSSP; P00747; 1CEA.
DR MEROPS; S01.977; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001152; HGF_MST1; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50948; PAN; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 704 AA; 79341 MW; CAB0D8CC41367C37 CRC64;

Query Match 45.9%; Score 1184; DB 2; Length 704;
Best Local Similarity 45.1%; Pred. No. 3.9e-81;
Matches 202; Conservative 72; Mismatches 150; Indels 24; Gaps 8;

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Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: :::|::   | |               | ||| ||         |:||  ::  :
Db         20 RSPLNDFQRLRGTELRAAPNEPPPSAPAHGAAQQCAQRCANRP----DCRAFHHERQSQL 75

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
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              |   |::  | | : :    :|||: ||::| ||:  | ||:||   |: |::|| | :
Db         76 CQLLPWSQRSPGARLQKNIHYDLYQKKDFLRECIVANGTSYRGTRDTTERGLRCQHWQAT 135

Qy        125 IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181
              ||:| :       |:|||||||  :: ||||:| :| ||:: | | :| :  |||||||
Db        136 TPHDHRFLPSLRNGLEENYCRNPDRDKRGPWCYTVDPNVRHQSCGIKKCEDAVCMTCNGE 195

Qy        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241
              ||| :|||||  |||| | ||:| : |::||:|| |||||||||   :|||| ||
Db        196 DYRGFVDHTESGTECQRWDLQHPHKHPYHPDKYPEKGLDDNYCRNPDSSEQPWCYTTDPA 255

Qy        242 TRWEYCAIKTCADNTMNDTDVPLE-TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              |:| |: |          |:  || | :|:|||||| ||   :|||||||:|  |
Db        256 LEREFCRIRVCKKRPR-----PINVTTGCYRGKGEGYRGRVNVTVSGIPCQRWDAQTLHR 310

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMS-HGQDCYRGN 359
              |   |  : ||||:||||||||||:|||||| | :|| :|  |  ||     ::|| |:
Db        311 HHFVPSKYPCKDLQENYCRNPDGSEAPWCFTTRPGMRVAFCFHIRRCDDELDAEECYHGH 370

Qy        360 GKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI-----FWEPDASKLNENYCRNPDDDAHGP 414
              |: | |::|:|| |:||  ||         |:        |:|  | :|||||||:|:|||
Db        371 GERYHGHVSKTRKGITCQRWDATTP----HVPQISPTTHPEA-HLEKNYCRNPDNDSHGP 425

Qy        415 WCYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||| :|  |:||| |  | |   |:::
Db        426 WCYTMDPRTPFDYCAIKPCSGSAVPSVL 453
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RESULT 14
HGFL_HUMAN
ID HGFL_HUMAN STANDARD; PRT; 711 AA.
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
DE stimulatory protein) (MSP) (Macrophage stimulating protein).
GN Name=MST1; Synonyms=HGFL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Friezner Degen S.J.;
RT "Characterization of the DNF15S2 locus on human chromosome 3:
RT identification of a gene coding for four kringle domains with homology
RT to hepatocyte growth factor.";
RL Biochemistry 30:9768-9780(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93340141; PubMed=8393443;
RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
RT "Cloning, sequencing, and expression of human macrophage stimulating
RT protein (MSP, MST1) confirms MSP as a member of the family of kringle
RT proteins and locates the MSP gene on chromosome 3.";
RL J. Biol. Chem. 268:15461-15468(1993).
RN [3]
RP SEQUENCE OF 230-247; 288-310; 326-341; 484-501; 530-549; 574-596 AND
RP 602-611, AND SUBUNIT.
RC TISSUE=Plasma;
RX PubMed=1827141;
RA Skeel A., Yoshimura T., Showalter S.D., Tanaka S., Appella E.,
RA Leonard E.J.;
RT "Macrophage stimulating protein: purification, partial amino acid
RT sequence, and cellular activity.";
RL J. Exp. Med. 173:1227-1234(1991).
CC -!- FUNCTION: Probably has no proteolytic activity, since crucial AA
CC characteristic of serine proteases catalytic sites are not
CC conserved.

```
CC   -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC       disulfide bond.
CC   -!- PTM: May be cleaved after Arg-483, to yield two chains held
CC       together by disulfide bonds, or two separate polypeptides.
CC   -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC       subfamily.
CC   -!- SIMILARITY: Contains 4 kringle domains.
CC   -!- SIMILARITY: Contains 1 PAN domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74178; AAA50165.1; -.
DR   EMBL; U37055; AAC50471.1; -.
DR   EMBL; L11924; AAA59872.1; -.
DR   PIR; A40331; A47136.
DR   HSSP; P00766; 1CHG.
DR   MEROPS; S01.975; -.
DR   Genew; HGNC:7380; MST1.
DR   MIM; 142408; -.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Direct protein sequencing; Glycoprotein; Kringle; Polymorphism;
KW   Repeat; Serine protease homolog; Signal.
FT   SIGNAL       1     18       Potential.
FT   CHAIN       19    711       Hepatocyte growth factor-like protein.
FT   DOMAIN      21    105       PAN.
FT   DOMAIN     110    186       Kringle 1.
FT   DOMAIN     191    268       Kringle 2.
FT   DOMAIN     283    361       Kringle 3.
FT   DOMAIN     370    448       Kringle 4.
FT   DOMAIN     484    711       Serine protease-like.
FT   DISULFID    56     78       By similarity.
FT   DISULFID    60     66       By similarity.
FT   DISULFID   110    186       By similarity.
FT   DISULFID   131    169       By similarity.
FT   DISULFID   157    181       By similarity.
FT   DISULFID   191    268       By similarity.
FT   DISULFID   194    324       Interchain (By similarity).
FT   DISULFID   212    251       By similarity.
FT   DISULFID   240    263       By similarity.
FT   DISULFID   283    361       By similarity.
FT   DISULFID   304    343       By similarity.
FT   DISULFID   332    355       By similarity.
FT   DISULFID   370    448       By similarity.
FT   DISULFID   391    431       By similarity.
FT   DISULFID   419    443       By similarity.
FT   DISULFID   468    588       Interchain (By similarity).
FT   DISULFID   507    523       By similarity.
FT   DISULFID   602    667       By similarity.
FT   DISULFID   632    646       By similarity.
FT   DISULFID   657    685       By similarity.
FT   CARBOHYD    72     72       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   615    615       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT     13     13       Y -> C.
FT                               /FTId=VAR_006631.
FT   VARIANT    212    212       C -> F.
FT                               /FTId=VAR_006632.
FT   VARIANT    676    676       E -> K (in dbSNP:7798).
FT                               /FTId=VAR_014569.
FT   CONFLICT   292    292       R -> G (in Ref. 3).
FT   CONFLICT   304    304       C -> E (in Ref. 3).
FT   CONFLICT   306    306       R -> E (in Ref. 3).
FT   CONFLICT   550    551       PS -> SL (in Ref. 3).
FT   CONFLICT   593    593       W -> E (in Ref. 3).
FT   CONFLICT   623    623       L -> F (in Ref. 2).
SQ   SEQUENCE   711 AA;  80379 MW;  596ED21F180290E4 CRC64;

  Query Match             45.4%;  Score 1171;  DB 1;  Length 711;
  Best Local Similarity   47.3%;  Pred. No. 3.8e-80;
  Matches  196;  Conservative   60;  Mismatches  148;  Indels   10;  Gaps    4;

Qy         33 VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKD 92
              |  |::|| ||    |    |:|| :: :   |   |:   |   :       ||:: ||
Db         50 VADAEECAGRC----GPLMDCRAFHYNVSSHGCQLLPWTQHSPHTRLRRSGRCDLFQKKD 105

Qy         93 YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSYR---GKDLQENYCRNPRGEEG 149
              |:| ||:  |  |:||::  |  |: || ||   |::| |       |:||:|||| |: |
Db        106 YVRTCIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNPDGDPG 165

Qy        150 GPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKF 209
              ||||:|::| ||:: | |  | |  |: |||| ||| :| ||||: ||||| | ||:| |
Db        166 GPWCYTTDPAVRFQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPF 225

Qy        210 LPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTEC 269
              | :: |:| ||||||||||  |||||| ||    |:| :  |        :   |  |
Db        226 EPGKFLDQGLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTVSC 283

Qy        270 IQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWC 329
              :|:|||||| ||   |:||||:| ||:|  ||| : |||||:|||||||:|||
Db        284 FRGKGEGYRGTANTTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDGSEAPWC 343

Qy        330 FTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHR 388
              ||  | :|  :| ||  | |    |||| | |: | | :|:|| |: |  |          :
Db        344 FTLRPGMRAAFCYQIRRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVQCQRWSAETPHKPQ 403

Qy        389 HIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV 442
                |      ::| ||:||||| |:|||||| :|  |:||| : ||  |  |:|:
Db        404 FTFTSEPHAQLEENFCRNPDGDSHGPWCYTMDPRTPFDYCALRRCADDQPPSIL 457


RESULT 15
P70006
ID   P70006      PRELIMINARY;      PRT;   717 AA.
AC   P70006;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hepatocyte growth factor-like protein precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96404125; PubMed=8808403; DOI=10.1016/0925-4773(95)00458-0;
RA   Aberger F., Schmidt G., Richter K.;
RT   "The Xenopus homologue of hepatocyte growth factor-like protein is
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RT   specifically expressed in the presumptive neural plate during
RT   gastrulation.";
RL   Mech. Dev. 54:23-37(1996).
DR   EMBL; Y08734; CAA69989.1; -.
DR   HSSP; P00746; 1FDP.
DR   MEROPS; S01.977; -.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004263; F:chymotrypsin activity; IEA.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0003809; F:thrombin activity; IEA.
DR   GO; GO:0004295; F:trypsin activity; IEA.
DR   GO; GO:0007596; P:blood coagulation; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011359; HGF_MST1.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR001254; Peptidase_S1.
DR   InterPro; IPR001314; Peptidase_S1A.
DR   InterPro; IPR003966; Peptidase_S1A_pr.
DR   InterPro; IPR009003; Pept_Ser_Cys.
DR   Pfam; PF00051; Kringle; 4.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; Trypsin; 1.
DR   PIRSF; PIRSF001152; HGF_MST1; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 4.
DR   SMART; SM00130; KR; 4.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 4.
DR   PROSITE; PS50070; KRINGLE_2; 4.
DR   PROSITE; PS50948; PAN; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
KW   Hydrolase; Kringle; Protease; Serine protease; Signal.
FT   SIGNAL        1     29       Potential.
FT   CHAIN        29    717       hepatocyte growth factor-like protein.
SQ   SEQUENCE   717 AA;  82017 MW;  6F877A432C8CDD54 CRC64;

  Query Match             45.1%;  Score 1163.5;  DB 2;  Length 717;
  Best Local Similarity   45.1%;  Pred. No. 1.4e-79;
  Matches  199;  Conservative   77;  Mismatches  152;  Indels   13;  Gaps    6;

Qy          5 RNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQ 64
              |: ::::::|    |: ::    :| :       || :|:        |::| ::   :
Db         32 RSALNDYQRSKGLELVHMNEG-GVKQEVQAEIQICAKQCSD----LLDCRSFDYNWKSQS 86

Qy         65 CLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSM 124
                |   |:   || |  :   ::|||: |||||:|::| | :|:|||| ||:|  || |
Db         87 CRLLPWTQNSSNVLLQRNVQYDLYQKKDYIRDCVVGNGNTYRGTVSKTKNGRTCQHWRLK 146

Qy        125 IPHEHSY---RGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181
               ||:| :      :|:|||||||  :  | ||:|::  :|:: | | :| :  |:|||||
Db        147 FPHDHKFSPTHWPELEENYCRNPDSDPEGLWCYTTDKNIRHQYCGIKKCEDAVCLTCNGE 206

Qy        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241
               ||| :| ||||| ||||| | || | : ||:|||| |||||||||   |||||| ||:
Db        207 DYRGSVDRTESGKECQRWDLQAPHTHPYKPEKYPDKSLDDNYCRNPDSSERPWCYTTDPN 266

Qy        242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH 301
                 |:| |  |    ::: ::   |: | : :|||||  ||  :||||||||:| || |
Db        267 VEREFCHITKCKKQRISNIEI---TSTCFKERGEGYRGKANTTTSGIPCQRWDTQAPHVH 323

Qy        302 DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNC-DMSHGQDCYRGNG 360
                 || : || | ||||||| |||:||||||  |:|: || ||  | |     :|| |||
Db        324 RFLPEKYPCKGLDENYCRNPVGSEAPWCFTTLKNMRMAYCFQIKRCTDDVVEPECYHGNG 383

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
               : | | :|:|| |: |  |::   ||   :  :|    | ||||||| |:|||||| :
Db        384 ELYRGRVSKTRKGIMCRRWEEKQNDLELSLA-QPYLVPLEENYCRNPDRDSHGPWCYTMD 442

Qy        421 PLIPWDYCPISRCEGDTTPTI 441
                |  |:||| :  | ||   |:
Db        443 PNTPFDYCALKPCAGDKVLTL 463


Search completed: October  3, 2005, 06:08:09
Job time : 64.6344 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:29 ; Search time 170.535 Seconds
(without alignments)
1002.420 Million cell updates/sec

Title: US-09-674-377B-2
Perfect score: 2579
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2576	99.9	442	7	ADM83267	Adm83267 Human NK4
2	2576	99.9	723	2	AAR07144	Aar07144 Tumour cy
3	2576	99.9	723	2	AAR15624	Aar15624 Human leu
4	2576	99.9	723	2	AAR25677	Aar25677 Recombina
5	2576	99.9	723	2	AAR57027	Aar57027 Human mod
6	2576	99.9	723	2	AAR57028	Aar57028 Human mod
7	2576	99.9	723	2	AAR57026	Aar57026 Human wil
8	2576	99.9	723	2	AAR82685	Aar82685 Tumour cy
9	2576	99.9	723	2	AAW76690	Aaw76690 Human pla
10	2576	99.9	729	2	AAY06621	Aay06621 HGF-MSP h
11	2576	99.9	729	2	AAY06622	Aay06622 HGF-MSP h
12	2576	99.9	1109	7	ADD69672	Add69672 Chimeric
13	2574	99.8	442	3	AAY57174	Aay57174 N-termina
14	2573	99.8	723	2	AAR21142	Aar21142 Human TCF
15	2566	99.5	723	2	AAW59923	Aaw59923 Human leu
16	2565	99.5	504	2	AAR32710	Aar32710 Haematopo
17	2563.5	99.4	447	7	ADE37393	Ade37393 Human hep
18	2563.5	99.4	447	7	ADM83266	Adm83266 Human NK4
19	2563.5	99.4	697	3	AAY98485	Aay98485 Hepatocyt
20	2563.5	99.4	697	3	AAY59030	Aay59030 Sequence
21	2563.5	99.4	697	4	AAB45838	Aab45838 Nucleic a
22	2563.5	99.4	697	4	AAU04275	Aau04275 Nuclear l
23	2563.5	99.4	728	2	AAR25676	Aar25676 Recombina
24	2563.5	99.4	728	2	AAR20005	Aar20005 Human hep
25	2563.5	99.4	728	2	AAR40862	Aar40862 Competati
26	2563.5	99.4	728	2	AAR40863	Aar40863 Competati
27	2563.5	99.4	728	2	AAR42062	Aar42062 Vascular
28	2563.5	99.4	728	2	AAR87522	Aar87522 Mutant he
29	2563.5	99.4	728	2	AAR87524	Aar87524 Mutant he
30	2563.5	99.4	728	2	AAR87525	Aar87525 Mutant he
31	2563.5	99.4	728	2	AAR87523	Aar87523 Mutant he
32	2563.5	99.4	728	2	AAW00340	Aaw00340 Wild type
33	2563.5	99.4	728	2	AAW00338	Aaw00338 Human hep
34	2563.5	99.4	728	2	AAW59922	Aaw59922 Human leu
35	2563.5	99.4	728	2	AAW58696	Aaw58696 Human hep
36	2563.5	99.4	728	2	AAW42998	Aaw42998 Recombina
37	2563.5	99.4	728	2	AAW39207	Aaw39207 Human hep
38	2563.5	99.4	728	6	ABP58128	Abp58128 Human hep
39	2563.5	99.4	728	7	ADB61534	Adb61534 Hepatocyt
40	2563.5	99.4	728	8	ADM97652	Adm97652 Human hep
41	2563.5	99.4	728	8	ADT89322	Adt89322 Human hep
42	2563.5	99.4	951	8	ADS19044	Ads19044 Chimeric
43	2561.5	99.3	447	3	AAY57173	Aay57173 N-termina
44	2557.5	99.2	727	2	AAR10656	Aar10656 Hepatic p
45	2557.5	99.2	728	2	AAR15623	Aar15623 Human leu

ALIGNMENTS

RESULT 1
ADM83267
ID ADM83267 standard; protein; 442 AA.
XX
AC ADM83267;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human NK4 protein #2.
XX
KW NK4 gene; neovascularisation; ovarian cancer; pancreatic cancer;
KW stomach cancer; gallbladder cancer; renal cancer; prostatic cancer;
KW breast cancer; esophageal cancer; hepatic cancer; oral cavity cancer;
KW colon cancer; colorectal cancer; sarcoma; glioma; melanoma; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN US2003162736-A1.
XX
PD 28-AUG-2003.
XX
PF 27-SEP-2002; 2002US-00255649.
XX
PR 25-FEB-2002; 2002JP-00048644.
XX
PA (NAKA/) NAKAMURA T.
PA (MATS/) MATSUMOTO K.
XX
PI Nakamura T, Matsumoto K;
XX
DR WPI; 2003-897946/82.
DR N-PSDB; ADM83265.
XX
PT New NK14 gene, useful for producing a medicament for preventing or
PT treating diseases caused by neovascularization, e.g. cancer.
XX
PS Disclosure; Page 17-19; 27pp; English.
XX
CC The present invention provides a therapeutic agent NK4 polypeptides and
CC their encoding polynucleotides. The invention is useful for producing a
CC medicament for preventing or treating diseases caused by
CC neovascularisation such as ovarian cancer, pancreatic cancer, stomach
CC cancer, gallbladder cancer, renal cancer, prostatic cancer, breast
CC cancer, esophageal cancer, hepatic cancer, oral cavity cancer, colon
CC cancer, colorectal cancer, sarcoma, glioma and melanoma. The invention is
CC also useful in gene therapy. The present sequence is human NK4 protein.
XX

```
SQ   Sequence 442 AA;

  Query Match             99.9%;  Score 2576;  DB 7;  Length 442;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-164;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
Db        421 PLIPWDYCPISRCEGDTTPTIV 442


RESULT 2
AAR07144
ID   AAR07144 standard; protein; 723 AA.
XX
AC   AAR07144;
XX
DT   25-MAR-2003  (revised)
DT   31-JAN-1991  (first entry)
XX
DE   Tumour cytotoxic factor II.
XX
KW   TCF II; glycoprotein; fibroblasts; anticancer agent.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .29
XX
PN   WO9010651-A.
XX
PD   20-SEP-1990.
XX
PF   10-MAR-1989;   89JP-00058631.
XX
PR   10-MAR-1989;   89JP-00058631.
PR   16-JAN-1990;   90JP-00006692.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Higashio K,  Mitsuda S,  Shima N,  Itagaki Y,  Nagao M;
XX
DR   WPI; 1990-304990/40.
DR   P-PSDB; AAR07144.
XX
PT   Human glyco:protein having antitumour activity - for inducing
PT   differentiation of leukaemia cells and enhancing cell mediated immunity.
XX
PS   Disclosure; Fig 15; 73pp; Japanese.
XX
CC   The sequence was deduced from the cDNA obtd. from a clone isolated from a
CC   cDNA library prepd. from RNA extd. from fibroblast IMR-90 cells (ATCC CCL
CC   -186). The N-terminal of the alpha chain is unclear. The sequence shows
CC   homology to hHGF except between AAs 162 and 166 of this sequence which is
CC   absent from the TCF-II sequence. The DNA can be used to produce the TCF
CC   II by recombinant DNA technology. TCF II is an anticancer agent and
CC   induces differentiation of leukaemia cells, enhances cell-mediated
CC   immunity, and accelerates the proliferation of human blood vessel
CC   endothelial cells and hepatic parenchymal cells. (Updated on 25-MAR-2003
CC   to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 3
AAR15624
ID   AAR15624 standard; protein; 723 AA.
XX
AC   AAR15624;
XX
DT   25-MAR-2003  (revised)
DT   18-MAR-1992  (first entry)
XX
DE   Human leukocyte-derived HGF encoded by clone HLC3.
XX
KW   Hepatocyte growth factor; liver; hepatoma.
XX
OS   Homo sapiens.
XX
PN   EP461560-A.
XX
```

PD 18-DEC-1991.
XX
PF 07-JUN-1991; 91EP-00109369.
XX
PR 11-JUN-1990; 90JP-00152474.
XX
PA (TOYM) TOYO BOSEKI KK.
XX
PI Nakamura T, Hagiya M, Seki T, Shimonishi M, Shimizu S, Ihara I;
PI Sakaguchi M, Asami O;
XX
DR WPI; 1991-370578/51.
DR N-PSDB; AAQ15177.
XX
PT Recombinant human leukocyte-derived hepatocyte growth factor - with DNA
PT encoding it, recombinant expression vectors and transformant cells
PT expressing it.
XX
PS Claim 3; Fig 3; 33pp; English.
XX
CC The sequence was deduced from a portion of HLC3, one of two clones, (for
CC HLC2 see AAR15623) isolated from a cDNA library prepd. from mRNA
CC extracted from human leukocytes. HLC2 has almost the same sequence as
CC HLC3 except for five residues (162-166) in HLC2 which do not appear in
CC HLC3. HLC3 shows similar characteristics to the human liver-derived HGF
CC identified in Nature, 342, 440, 1989, but differs at 14 positions in the
CC amino acid sequence. The DNA sequence can be expressed and the resulting
CC protein, recombinant HGF, used in hepa- tocyte cultivation, liver
CC regeneration, hepatocyte research, esp. into the mechanism of hepatoma,
CC and to prepare anti-HGF antibodies for diagnosis and therapy. (Updated on
CC 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 723 AA;

Query Match 99.9%; Score 2576; DB 2; Length 723;
Best Local Similarity 99.8%; Pred. No. 1.4e-163;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473
```

RESULT 4
AAR25677

ID AAR25677 standard; protein; 723 AA.
XX
AC AAR25677;
XX
DT 20-JAN-1993 (first entry)
XX
DE Recombinant human hepatocyte growth factor.
XX
KW HGF; enhance growth; preparing transgenic animals; hepatic disease;
KW clinical diagnostic reagent; drug.
XX
OS Homo sapiens.
XX
PN JP04183394-A.
XX
PD 30-JUN-1992.
XX
PF 19-NOV-1990; 90JP-00314548.
XX
PR 19-NOV-1990; 90JP-00314548.
XX
PA (TOYM) TOYOBO KK.
PA (NAKA/) NAKAMURA T.
XX
DR WPI; 1992-265591/32.
XX
PT Recombinant human hepatocyte growth factor and DNA encoding it - useful
PT for diagnosis and treatment of hepatic disease and transgenic animal
PT prepn.
XX
PS Disclosure; Page 13; 28pp; Japanese.
XX
CC This sequence represents a recombinant human hepatocyte growth factor. It
CC has physiological activity, and using it enhanced growth of hepatocytes
CC is possible. It is useful as a clinical diagnostic reagent, or a drug for
CC treating hepatic disease. See also AAR25676-92, AAQ26713-27
XX
SQ Sequence 723 AA;

Query Match 99.9%; Score 2576; DB 2; Length 723;
Best Local Similarity 99.8%; Pred. No. 1.4e-163;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
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Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 5
AAR57027
ID   AAR57027 standard; protein; 723 AA.
XX
AC   AAR57027;
XX
DT   25-MAR-2003  (revised)
DT   19-MAR-1995  (first entry)
XX
DE   Human modified tumor cytotoxic factor.
XX
KW   Tumor cytotoxic factor; hepatocyte growth factor; antitumor.
XX
OS   Homo sapiens.
XX
PN   WO9414845-A1.
XX
PD   07-JUL-1994.
XX
PF   27-DEC-1993;   93WO-JP001905.
XX
PR   28-DEC-1992;   92JP-00359747.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Yamaguchi K,  Shima N,  Murakami A,  Goto M,  Tsuda E,  Masunaga H;
PI   Takahira R,  Oogaki F,  Ueda M,  Higashio K;
XX
DR   WPI; 1994-234619/28.
XX
PT   Modified tumour cytotoxic factors with loss of binding of N-linked
PT   oligosaccharide chain - have longer biological half-life without loss of
PT   biological activity.
XX
PS   Claim 5; Page 33; 59pp; English.
XX
CC   This modified TCF sequence has a prolonged biological half-life without
CC   any loss of biological activity, is obtained by altering the amino acid
CC   residue at position 563 from Ser in the wild-type to Ala. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              ||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 6
AAR57028
ID   AAR57028 standard; protein; 723 AA.
XX
AC   AAR57028;
XX
DT   25-MAR-2003  (revised)
DT   19-MAR-1995  (first entry)
XX
DE   Human modified tumor cytotoxic factor.
XX
KW   Tumor cytotoxic factor; hepatocyte growth factor; antitumor.
XX
OS   Homo sapiens.
XX
PN   WO9414845-A1.
XX
PD   07-JUL-1994.
XX
PF   27-DEC-1993;   93WO-JP001905.
XX
PR   28-DEC-1992;   92JP-00359747.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Yamaguchi K,  Shima N,  Murakami A,  Goto M,  Tsuda E,  Masunaga H;
PI   Takahira R,  Oogaki F,  Ueda M,  Higashio K;
XX
DR   WPI; 1994-234619/28.
XX
PT   Modified tumour cytotoxic factors with loss of binding of N-linked
PT   oligosaccharide chain - have longer biological half-life without loss of
PT   biological activity.
XX
PS   Claim 6; Page 33; 59pp; English.
XX
CC   This modified TCF sequence has a prolonged biological half-life without
CC   any loss of biological activity, is obtained by altering the amino acid
CC   residue at position 563 from Ser in the wild-type to Ala. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271
```

```
Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473
```

RESULT 7
AAR57026
ID AAR57026 standard; protein; 723 AA.
XX
AC AAR57026;
XX
DT 25-MAR-2003 (revised)
DT 19-MAR-1995 (first entry)
XX
DE Human wild-type tumor cytotoxic factor.
XX
KW Tumor cytotoxic factor; hepatocyte growth factor; antitumor.
XX
OS Homo sapiens.
XX
PN WO9414845-A1.
XX
PD 07-JUL-1994.
XX
PF 27-DEC-1993; 93WO-JP001905.
XX
PR 28-DEC-1992; 92JP-00359747.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Yamaguchi K, Shima N, Murakami A, Goto M, Tsuda E, Masunaga H;
PI Takahira R, Oogaki F, Ueda M, Higashio K;
XX
DR WPI; 1994-234619/28.
XX
PT Modified tumour cytotoxic factors with loss of binding of N-linked
PT oligosaccharide chain - have longer biological half-life without loss of
PT biological activity.
XX
PS Disclosure; Page 29; 59pp; English.
XX
CC This TCF sequence may be modified in that the AA residues responsible for
CC binding of N-linked oligosaccharide chains are modified so that at least
CC one of the N-linked oligosaccharide chains is prevented from binding to
CC TCF. Ser-563 may be substituted with Ala (AAR57027) or Asn-289
CC substituted with Gln (AAR57028). (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 723 AA;

```
  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473
```

RESULT 8
AAR82685
ID AAR82685 standard; protein; 723 AA.
XX
AC AAR82685;
XX
DT 24-APR-1996 (first entry)
XX
DE Tumour cytotoxic factor-II.
XX
KW Tumour cytotoxic factor-II; TCF-II; hepatocyte growth factor; HGF;
KW monoclonal antibody; MAb; hybridoma; antitumour agent.
XX
OS Homo sapiens.
XX
PN EP672685-A2.
XX
PD 20-SEP-1995.
XX
PF 17-MAR-1995; 95EP-00301800.
XX
PR 18-MAR-1994; 94JP-00074263.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Higashio K, Shima N, Oogaki F;
XX
DR WPI; 1995-329569/43.
XX
PT Monoclonal antibody to human tumour cytotoxic factor-II - has no affinity
PT to human hepatocyte growth factor, is used for specific determn. or
PT purification of TCF-II.
XX
PS Disclosure; Page 14-17; 19pp; English.
XX
CC This sequence represents human tumour cytotoxic factor-II (TCF-II). TCF-
CC II has potent antitumour activity and growth stimulation activity. TCF-II
CC is a member of the hepatocyte growth factor family (HGF). This sequence
CC is used as an antigen to produce TCF-II specific antibodies that show no
CC affinity to human HGF. The monoclonal antibody (MAb) was produced using
CC hybridoma techniques. The MAbs were screened using solid phase ELISA with
CC an increased selectivity. The MAb can be used for the selective
CC determination or purification of TCF-II without any influence from the
CC presence of HGF. The TCF-II can be used as an antitumour agent, a wound
CC healing agent and as a marker for the diagnosis of diseases
XX
SQ Sequence 723 AA;

```
  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 9
AAW76690
ID   AAW76690 standard; protein; 723 AA.
XX
AC   AAW76690;
XX
DT   25-MAR-2003  (revised)
DT   29-JAN-1999  (first entry)
XX
DE   Human plasminogen-like growth factor.
XX
KW   Human; plasminogen-like growth factor; PLGF; endothelial cell;
KW   epithelial cell; splice variant; wound healing.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 175
FT                   /note= "Encoded by ACT"
XX
PN   US5821223-A.
XX
PD   13-OCT-1998.
XX
PF   05-MAY-1994;   94US-00238742.
XX
PR   14-SEP-1990;   90US-00582063.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Aaronson SA,  Rubin JS,  Chan AM;
XX
DR   WPI; 1998-567711/48.
DR   N-PSDB; AAV61952.
XX
PT   Stimulation of endothelial or epithelial cell growth - with plasminogen-
PT   like growth factor protein.
XX
PS   Claim 3; Fig 4C; 19pp; English.
XX
CC   The Human plasminogen-like growth factor PLGF is used in the stimulation
CC   of the growth of endothelial cells or epithelial cells other than
CC   hepatocytes. This involves contacting the cells with the PLGF protein or
CC   its allelic or splice variants. The growth factor is useful for
CC   stimulating wound healing in endothelial or epithelial tissue. (Updated
CC   on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 10
AAY06621
ID   AAY06621 standard; protein; 729 AA.
XX
AC   AAY06621;
XX
DT   26-OCT-1999  (first entry)
XX
DE   HGF-MSP hybrid protein alphabet-1 factor.
XX
KW   Alphabet-1; human; hepatocyte growth factor; HGF; MSP;
KW   macrophage stimulating protein; apoptosis; chemotherapy; toxicity;
KW   therapy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .487
FT                   /note= "HGF alpha chain"
FT   Peptide         1. .31
FT                   /note= "HSP alpha signal peptide"
```

```
FT   Protein         32. .729
FT                   /note= "mature protein"
FT   Cleavage-site   488. .491
FT                   /note= "HGF cleavage site"
FT   Domain          492. .717
FT                   /note= "MSP beta chain"
FT   Peptide         718. .729
FT                   /note= "polyhistidine tag"
XX
PN   WO9938968-A1.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-EP000502.
XX
PR   30-JAN-1998;   98IT-MI000180.
XX
PA   (DOMP-) DOMPE SPA.
XX
PI   Medico E,  Michieli P,  Collesi C,  Caselli G,  Comoglio P;
XX
DR   WPI; 1999-494091/41.
DR   N-PSDB; AAX87676.
XX
PT   Recombinant proteins from recombination of HGF and MSP structural
PT   domains, useful for protecting cells against apoptosis induced by
PT   chemotherapeutics.
XX
PS   Example 1; Page 54-56; 63pp; English.
XX
CC   This is the amino acid sequence of alphabet-1 factor, a recombinant
CC   protein composed of the hepatocyte growth factor (HGF) alpha chain (i.e.
CC   the signal sequence, hairpin loop and kringles 1-4), the natural cleavage
CC   site of HGF, the macrophage stimulating protein (MSP) beta chain and a
CC   polyhistidine tag sequence. This structure allows the recombinant protein
CC   to interact with both the HGF receptor (Met) and the MSP receptor (Ron)
CC   and thereby induce biological responses which are synergistic and
CC   selective compared with the natural factor and truncated forms of the
CC   proteins. The portions of DNA encoding the various portions of alphabet-1
CC   are obtained by PCR amplification of HGF or MSP cDNA and recombined to
CC   obtain a hybrid DNA (see AAX87676). Expression vectors, prokaryotic or
CC   eukaryotic host cells and a process for preparing recombinant proteins
CC   from HGF and MSP are claimed. Alphabet-1 and other HGF-MSP recombinant
CC   proteins are used for the prevention or treatment of chemotherapeutic-
CC   induced toxicity such as myelotoxicity, hepatotoxicity, nephrotoxicity,
CC   mucotoxicity and neurotoxicity (claimed). They protect cells from death
CC   (apoptosis) induced by chemotherapy of, e.g. tumors. In particular, they
CC   can be used for expansion of marrow precursors, to increase proliferation
CC   of the haematopoietic precursors or to stimulate their entry in the
CC   cycle. By modification of the proteolytic site, hybrid factors can be
CC   obtained which are activated by proteases of the endoplasmic reticulum
CC   (such as furines) during their synthesis. When the proteolytic site is
CC   removed, permanently immature forms of the factors can be obtained,
CC   having a potential partial agonistic or antagonistic activity. Different
CC   functional domains can be combined so as to modulate the biological
CC   effects
XX
SQ   Sequence 729 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 729;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 11
AAY06622
ID   AAY06622 standard; protein; 729 AA.
XX
AC   AAY06622;
XX
DT   26-OCT-1999  (first entry)
XX
DE   HGF-MSP hybrid protein alphabet-RTKR factor.
XX
KW   Alphabet-RTKR; human; hepatocyte growth factor; HGF; MSP;
KW   macrophage stimulating protein; apoptosis; chemotherapy; toxicity;
KW   therapy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .483
FT                   /note= "HGF alpha chain"
FT   Peptide         1. .31
FT                   /note= "HSP alpha signal peptide"
FT   Protein         32. .729
FT                   /note= "mature protein"
FT   Cleavage-site   484. .487
FT                   /note= "furine protease cleavage site"
FT   Cleavage-site   488. .491
FT                   /note= "HGF cleavage site"
FT   Domain          492. .717
FT                   /note= "MSP beta chain"
FT   Peptide         718. .729
FT                   /note= "polyhistidine tag"
XX
PN   WO9938968-A1.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-EP000502.
XX
PR   30-JAN-1998;   98IT-MI000180.
XX
PA   (DOMP-) DOMPE SPA.
XX
PI   Medico E,  Michieli P,  Collesi C,  Caselli G,  Comoglio P;
XX
DR   WPI; 1999-494091/41.
DR   N-PSDB; AAX87677.
XX
PT   Recombinant proteins from recombination of HGF and MSP structural
PT   domains, useful for protecting cells against apoptosis induced by
```

```
PT   chemotherapeutics.
XX
PS   Example 2; Page 58-60; 63pp; English.
XX
CC   This is the amino acid sequence of alphabet-RTKR factor, a recombinant
CC   protein composed of the hepatocyte growth factor (HGF) alpha chain (i.e.
CC   the signal sequence, hairpin loop and kringles 1-4), a furine protease
CC   cleavage site, the natural cleavage site of HGF, the macrophage
CC   stimulating protein (MSP) beta chain and a polyhistidine tag sequence.
CC   This structure allows the recombinant protein to interact with both the
CC   HGF receptor (Met) and the MSP receptor (Ron) and thereby induce
CC   biological responses which are synergistic and selective compared with
CC   the natural factor and truncated forms of the proteins. The portions of
CC   DNA encoding the various portions of alphabet-RTKR are obtained by PCR
CC   amplification of HGF or MSP cDNA and recombined to obtain a hybrid DNA
CC   (see AAX87677). Expression vectors, prokaryotic or eukaryotic host cells
CC   and a process for preparing recombinant proteins from HGF and MSP are
CC   claimed. Alphabet-RTKR and other HGF-MSP recombinant proteins are used
CC   for the prevention or treatment of chemotherapeutic-induced toxicity such
CC   as myelotoxicity, hepatotoxicity, nephrotoxicity, mucotoxicity and
CC   neurotoxicity (claimed). They protect cells from death (apoptosis)
CC   induced by chemotherapy of, e.g. tumors. In particular, they can be used
CC   for expansion of marrow precursors, to increase proliferation of the
CC   haematopoietic precursors or to stimulate their entry in the cycle. By
CC   modification of the proteolytic site, hybrid factors can be obtained
CC   which are activated by proteases of the endoplasmic reticulum (such as
CC   furines) during their synthesis. When the proteolytic site is removed,
CC   permanently immature forms of the factors can be obtained, having a
CC   potential partial agonistic or antagonistic activity. Different
CC   functional domains can be combined so as to modulate the biological
CC   effects
XX
SQ   Sequence 729 AA;

  Query Match             99.9%;  Score 2576;  DB 2;  Length 729;
  Best Local Similarity   99.8%;  Pred. No. 1.4e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 12
ADD69672
ID   ADD69672 standard; protein; 1109 AA.
XX
AC   ADD69672;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Chimeric HGF/HBsAg L protein - SEQ ID 20.
XX
KW   hollow nanoparticle; HBV surface antigen protein; HBsAg L; hepatotropic;
KW   liver disease; gene therapy; chimeric; HGF.
XX
OS   Unidentified.
OS   Hepatitis B virus.
XX
PN   WO2003082345-A1.
XX
PD   09-OCT-2003.
XX
PF   05-MAR-2003; 2003WO-JP002602.
XX
PR   29-MAR-2002; 2002JP-00097280.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kuroda S,  Tanizawa K,  Kondo A,  Ueda M,  Seno M,  Tada H;
XX
DR   WPI; 2003-803976/75.
DR   N-PSDB; ADD69671.
XX
PT   Drugs comprising protein to form hollow nanoparticles with therapeutic
PT   substances encapsulated capable of recognizing target cells or tissues
PT   specifically and selectively, applicable in disease treatment.
XX
PS   Example F; SEQ ID NO 20; 109pp; Japanese.
XX
CC   The invention relates to a novel drug comprising a protein forming hollow
CC   nanoparticles and capable of recognising specific cells which is fused
CC   with therapeutic substances for transfer into cells. The protein is
CC   particularly hepatitis B virus (HBV) surface antigen protein (HBsAg). The
CC   drugs of the invention demonstrate hepatotropic activity and may be
CC   useful for disease treatment, particularly in the therapy of liver
CC   diseases. The protein of the invention and subsequently the drug, has
CC   selectivity and specificity in targeting cells or tissues for delivering
CC   drugs fused with the specific nanoparticle-forming proteins, therefore,
CC   gene therapy can be achieved without needing surgery and with reduced
CC   side-effects. The current sequence is that of the chimeric HGF/HBsAg L
CC   protein (SEQ ID 20) of the invention.
XX
SQ   Sequence 1109 AA;

  Query Match             99.9%;  Score 2576;  DB 7;  Length 1109;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-163;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 477

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 537

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 597

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 657

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 717
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Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 777

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 837

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        838 PLIPWDYCPISRCEGDTTPTIV 859


RESULT 13
AAY57174
ID   AAY57174 standard; protein; 442 AA.
XX
AC   AAY57174;
XX
DT   11-FEB-2000  (first entry)
XX
DE   N-terminal region of alpha-chain of HGF mutant (residues 32-478).
XX
KW   Neovascularization; inhibitor; hepatocyte growth factor; HGF;
KW   cMet-HGF receptor; rheumatoid arthritis; diabetic conjunctivitis;
KW   neonatal conjunctivitis; senile macular degeneration; scarring; mutant;
KW   wound healing; contraceptive; vascularization; Crohn's disease; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   1
FT                   /note= "pyroglutamate"
FT   Peptide         130. .131
FT                   /note= "deletion of 5 amino acids (see AAY57173)"
XX
PN   WO9955361-A1.
XX
PD   04-NOV-1999.
XX
PF   06-APR-1999;   99WO-JP001834.
XX
PR   28-APR-1998;   98JP-00134681.
XX
PA   (NAKA/) NAKAMURA T.
XX
PI   Nakamura T;
XX
DR   WPI; 2000-023263/02.
XX
PT   Neovascularization inhibitory factors and neovascularization inhibitors,
PT   for preventing or treating, e.g. rheumatoid arthritis and diabetic
PT   conjunctivitis.
XX
PS   Claim 5; Page 69-72; 78pp; Japanese.
XX
CC   The invention relates to neovascularization inhibitors comprising a
CC   polypeptide (A) with the amino acid sequence of N-terminal region of
CC   hepatocyte growth factor (HGF), or a polypeptide with an amino acid
CC   sequence derived from (A) which has antagonistic activity against HGF via
CC   the cMet-HGF receptor. The polypeptides can be used as neovascularization
CC   inhibitory factors (e.g. for preventing and treating rheumatoid
CC   arthritis, diabetic conjunctivitis, neonatal conjunctivitis, senile
CC   macular degeneration and excess scarring during wound healing), as a
CC   contraceptive, to modulate abnormal proliferation or vascularization
CC   (e.g. psoriasis, Osler-Webber syndrome, myocardiac angiopoiesis,
CC   peripheral angiectasis, haemophiliac rheumatism, angiopoiesis of the eye,
CC   angiofibroma, benign tumor and wound granulation), or to treat or prevent
CC   conditions due to the over-stimulation of endothelial cells (e.g. Crohn's
CC   disease, adenomatous sclerosis, gastrointestinal healing, toughening of
CC   skin and excess scarring). The present sequence represents the N-terminal
CC   region of alpha-chain of human HGF with a deletion of 5 amino acids
CC   between residues 130 -131 of the present sequence
XX
SQ   Sequence 442 AA;

  Query Match             99.8%;  Score 2574;  DB 3;  Length 442;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-163;
  Matches  441;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKA 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 RKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKA 61

Qy         62 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 121

Qy        122 SSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGE 181

Qy        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 SYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPH 241

Qy        242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEH 301

Qy        302 DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGK 361
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 DMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGK 361

Qy        362 NYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNP 421
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 NYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNP 421

Qy        422 LIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        422 LIPWDYCPISRCEGDTTPTIV 442


RESULT 14
AAR21142
ID   AAR21142 standard; protein; 723 AA.
XX
AC   AAR21142;
XX
DT   25-MAR-2003  (revised)
DT   20-MAY-1992  (first entry)
XX
DE   Human TCF-II.
XX
KW   Tumour cell killing factor; hepatocyte growth factor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          490. .505
FT                   /note= "Beta-chain N-terminal sequence"
XX
PN   WO9201053-A.
XX
PD   23-JAN-1992.
XX
PF   13-JUL-1990;   90JP-00185852.
XX
PR   13-JUL-1990;   90JP-00185852.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Shima N,  Higashio K,  Nagao M,  Oogaki F,  Takaoka H,  Tsuda E;
XX
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DR   WPI; 1992-056868/07.
DR   N-PSDB; AAQ21066.
XX
PT   Prodn. of liver cell growth factor TCF-II - by culture of a transformant
PT   contg. cdna for tcf-11 and deriving from human foetal lung fibroblast
PT   cells.
XX
PS   Claim 6; Fig 1; 47pp; Japanese.
XX
CC   A human foetal lung fibroblast library was screened with a synthetic
CC   probe coding for the N-terminal sequence of TCF-II. A cDNA clone was
CC   isolated and sequenced. The coding sequence can be incorporated into a
CC   plasmid and transformed into a microorganism for production of TCF- II.
CC   The protein itself can be used as a liver cell growth factor or a tumour
CC   cell killing factor. See also AAQ21067-9. (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.8%;  Score 2573;  DB 2;  Length 723;
  Best Local Similarity   99.5%;  Pred. No. 2.3e-163;
  Matches  440;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGMKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 15
AAW59923
ID   AAW59923 standard; protein; 723 AA.
XX
AC   AAW59923;
XX
DT   25-MAR-2003  (revised)
DT   21-DEC-1998  (first entry)
XX
DE   Human leukocyte-derived hepatocyte growth factor HCL2.
XX
KW   Hepatocyte-derived growth factor; HGF; human; liver; hepatoma; diagnosis;
KW   therapy.
XX
OS   Homo sapiens.
XX
PN   EP859009-A2.
XX
PD   19-AUG-1998.
XX
PF   07-JUN-1991;   98EP-00108130.
XX
PR   11-JUN-1990;   90JP-00152474.
PR   07-JUN-1991;   91EP-00109369.
XX
PA   (NAKA/) NAKAMURA T.
XX
PI   Nakamura T,  Hagiya M,  Seki T,  Shimonishi M,  Shimizu S,  Ihara I;
PI   Sakaguchi M,  Asami O;
XX
DR   WPI; 1998-429650/37.
DR   N-PSDB; AAV53627.
XX
PT   Preparation of recombinant hepatocyte growth factor polypeptide - by
PT   culturing mammalian cells transformed with vector containing human
PT   leukocyte-derived HGF gene.
XX
PS   Example 1; Fig 3a-c; 30pp; English.
XX
CC   This is the amino acid sequence for human leukocyte-derived hepatocyte
CC   growth factor (HGF) HLC2, deduced from a cDNA clone (see AAV53627)
CC   obtained from a leukocyte cDNA library. Another leukocyte-derived HGF,
CC   HLC3 (see AAW59924), was identified that differs from HLC3 by having an
CC   extra 5 amino acid residues. A claimed method of producing a HGF
CC   comprises: transforming mammalian cells (preferably CHO cells) with a
CC   recombinant expression vector that has a promoter (preferably the SV40
CC   early promoter), a gene coding for human leukocyte-derived HGF, and the
CC   dihydrofolate reductase gene; (b) culturing the transformed cells in the
CC   presence of successively elevated concentrations of methotrexate; and (c)
CC   recovering the HGF polypeptide from the culture supernatant. HGF
CC   polypeptides may be used as hepatocyte cultivation reagents, liver
CC   regeneration promoters, in basic research on liver function, research on
CC   the action of various hormones and drugs on hepatocytes, research on the
CC   carcinogenesis mechanism of hepatoma, clinical diagnostic reagents using
CC   an antibody against the polypeptide and therapeutic drugs for liver
CC   disease. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR
CC   -2003 to correct PR field.)
XX
SQ   Sequence 723 AA;

  Query Match             99.5%;  Score 2566;  DB 2;  Length 723;
  Best Local Similarity   99.3%;  Pred. No. 6.6e-163;
  Matches  439;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYSGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
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Db        392 KNYMGNLSQTRSGLTCSIWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              ||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 06:06:02 ; Search time 239.645 Seconds
(without alignments)
765.639 Million cell updates/sec

Title: US-09-674-377B-2
Perfect score: 2579
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2576	99.9	489	18	US-10-926-088A-2	Sequence 2, Appli
2	2576	99.9	723	8	US-08-605-221-4	Sequence 4, Appli
3	2576	99.9	1109	18	US-10-509-247A-20	Sequence 20, Appl
4	2563.5	99.4	447	9	US-09-951-629-1	Sequence 1, Appli
5	2563.5	99.4	447	14	US-10-081-309-2	Sequence 2, Appli
6	2563.5	99.4	494	18	US-10-926-088A-1	Sequence 1, Appli
7	2563.5	99.4	726	17	US-10-872-198-120	Sequence 120, App
8	2563.5	99.4	726	20	US-11-021-951-120	Sequence 120, App
9	2563.5	99.4	728	8	US-08-605-221-2	Sequence 2, Appli
10	2563.5	99.4	728	16	US-10-813-805-10	Sequence 10, Appl
11	2563.5	99.4	728	16	US-10-475-616-2	Sequence 2, Appli
12	2563.5	99.4	728	17	US-10-498-332-7	Sequence 7, Appli
13	2554	99.0	723	13	US-10-133-912-18	Sequence 18, Appl
14	2552	99.0	723	13	US-10-133-912-19	Sequence 19, Appl
15	2527.5	98.0	727	16	US-10-149-103A-1	Sequence 1, Appli
16	2435.5	94.4	475	16	US-10-275-296-14	Sequence 14, Appl
17	2435.5	94.4	482	16	US-10-275-296-13	Sequence 13, Appl
18	2435.5	94.4	566	16	US-10-275-296-2	Sequence 2, Appli
19	2430	94.2	725	14	US-10-311-776-4	Sequence 4, Appli
20	2427	94.1	723	15	US-10-297-158-4	Sequence 4, Appli
21	2417.5	93.7	730	14	US-10-311-776-2	Sequence 2, Appli
22	2414.5	93.6	728	15	US-10-297-158-2	Sequence 2, Appli
23	2370.5	91.9	727	16	US-10-813-805-12	Sequence 12, Appl
24	2096.5	81.3	368	16	US-10-149-103A-3	Sequence 3, Appli
25	1550.5	60.1	269	16	US-10-149-103A-2	Sequence 2, Appli
26	1433.5	55.6	290	14	US-10-283-769-8	Sequence 8, Appli
27	1171	45.4	670	15	US-10-210-130-152	Sequence 152, App
28	1171	45.4	706	18	US-10-450-763-49987	Sequence 49987, A
29	1171	45.4	711	10	US-09-849-138-42	Sequence 42, Appl
30	1171	45.4	711	10	US-09-981-151A-51	Sequence 51, Appl
31	1171	45.4	711	10	US-09-981-151A-52	Sequence 52, Appl
32	1171	45.4	711	10	US-09-981-151A-53	Sequence 53, Appl
33	1171	45.4	711	11	US-09-972-211-132	Sequence 132, App
34	1171	45.4	711	11	US-09-972-211-133	Sequence 133, App
35	1171	45.4	711	11	US-09-972-211-134	Sequence 134, App
36	1171	45.4	711	14	US-10-123-036-2	Sequence 2, Appli
37	1171	45.4	711	15	US-10-116-275-229	Sequence 229, App
38	1171	45.4	711	15	US-10-004-378A-118	Sequence 118, App
39	1171	45.4	711	15	US-10-004-378A-119	Sequence 119, App
40	1171	45.4	711	15	US-10-004-378A-120	Sequence 120, App
41	1171	45.4	711	15	US-10-096-625-132	Sequence 132, App
42	1171	45.4	711	15	US-10-096-625-133	Sequence 133, App
43	1171	45.4	711	15	US-10-096-625-134	Sequence 134, App
44	1171	45.4	711	16	US-10-409-554-2	Sequence 2, Appli
45	1166.5	45.2	710	16	US-10-149-103A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-926-088A-2
; Sequence 2, Application US/10926088A
; Publication No. US20050164918A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA Toshikazu
; APPLICANT: MATSUMOTO Kunio
; APPLICANT: FUKUTA Kazuhiro
; TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
; FILE REFERENCE: 2004-1328A/WMC/01736
; CURRENT APPLICATION NUMBER: US/10/926,088A
; CURRENT FILING DATE: 2004-08-26
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: alpha-chain of human hepatocyte growth factor of five amino acid
; OTHER INFORMATION: type
US-10-926-088A-2

Query Match 99.9%; Score 2576; DB 18; Length 489;
Best Local Similarity 99.8%; Pred. No. 9.6e-210;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-605-221-4
; Sequence 4, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Toshikazu
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
; FILE REFERENCE: 2520-0101P
; CURRENT APPLICATION NUMBER: US/08/605,221
; CURRENT FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HGF-B (five amino acids deletion type)
US-08-605-221-4

Query Match 99.9%; Score 2576; DB 8; Length 723;
Best Local Similarity 99.8%; Pred. No. 1.5e-209;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
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RESULT 3
US-10-509-247A-20
; Sequence 20, Application US/10509247A
; Publication No. US20050181064A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; APPLICANT: Kuroda, Shunichi
; APPLICANT: Tanizawa, Katsuyuki
; APPLICANT: Kondo, Akihiko
; APPLICANT: Ueda, Masakazu
; APPLICANT: Seno, Masaharu
; APPLICANT: Tada, Hiroko
; TITLE OF INVENTION: DRUG CONTAINING HOLLOW PROTEIN NANOPARTICLES OF PARTICLE-FORMING
; TITLE OF INVENTION: PROTEIN, FUSED WITH DISEASE-TREATING TARGET-CELL-SUBSTANCE
; FILE REFERENCE: P023P01/US
; CURRENT APPLICATION NUMBER: US/10/509,247A
; CURRENT FILING DATE: 2004-09-28
; PRIOR APPLICATION NUMBER: PCT/JP03/02602
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: JP2002-97280
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-509-247A-20

Query Match 99.9%; Score 2576; DB 18; Length 1109;
Best Local Similarity 99.8%; Pred. No. 2.6e-209;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
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Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
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Db        838 PLIPWDYCPISRCEGDTTPTIV 859


RESULT 4
US-09-951-629-1
; Sequence 1, Application US/09951629
; Publication No. US20020004480A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA, Toshikazu
;  TITLE OF INVENTION: Anti-Cancer Agent
;  FILE REFERENCE: 4373-0101P
;  CURRENT APPLICATION NUMBER: US/09/951,629
;  CURRENT FILING DATE:  2001-09-14
;  PRIOR APPLICATION NUMBER: JP 300728
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: PCT/JP96/03105
;  PRIOR FILING DATE: 1996-10-23
;  PRIOR APPLICATION NUMBER: US 09/471,032
;  PRIOR FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-951-629-1

  Query Match             99.4%;  Score 2563.5;  DB 9;  Length 447;
  Best Local Similarity   98.7%;  Pred. No. 9.9e-209;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
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Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
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Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
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Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
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Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
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Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 5
US-10-081-309-2
; Sequence 2, Application US/10081309
; Publication No. US20030012775A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffmann-La Roche Inc.
;  TITLE OF INVENTION: PEG Conjugates of NK4
;  FILE REFERENCE: 20859
;  CURRENT APPLICATION NUMBER: US/10/081,309
;  CURRENT FILING DATE:  2002-06-04
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: homosapiens
US-10-081-309-2

  Query Match             99.4%;  Score 2563.5;  DB 14;  Length 447;
  Best Local Similarity   98.7%;  Pred. No. 9.9e-209;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
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Db        121 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 180

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
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Db        181 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 240

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
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Db        241 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 300

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 360

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 420

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        421 CYTGNPLIPWDYCPISRCEGDTTPTIV 447


RESULT 6
US-10-926-088A-1
; Sequence 1, Application US/10926088A
; Publication No. US20050164918A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAMURA Toshikazu
;  APPLICANT:  MATSUMOTO Kunio
;  APPLICANT:  FUKUTA Kazuhiro
;  TITLE OF INVENTION: A segment of glycosylation-deficient HGF alpha-chain
;  FILE REFERENCE: 2004-1328A/WMC/01736
;  CURRENT APPLICATION NUMBER: US/10/926,088A
;  CURRENT FILING DATE:  2004-08-26
;  NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
;   LENGTH: 494
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   OTHER INFORMATION: alpha-chain of human hepatocyte growth factor
US-10-926-088A-1

  Query Match             99.4%;  Score 2563.5;  DB 18;  Length 494;
  Best Local Similarity   98.7%;  Pred. No. 1.1e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 7
US-10-872-198-120
; Sequence 120, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
;  APPLICANT: Ulrich HAUPTS
;  APPLICANT:  Andre KOLTERMANN
;  APPLICANT:  Andreas SCHEIDIG
;  APPLICANT:  Christian VOETSMEIER
;  APPLICANT:  Ulrich Kettling
;  TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
;  FILE REFERENCE: 04156.0002U4
;  CURRENT APPLICATION NUMBER: US/10/872,198
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: 60/543,518
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/524,960
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: EP 04003058
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: EP 03025871
;  PRIOR FILING DATE: 2003-11-11
;  PRIOR APPLICATION NUMBER: EP 03025851
;  PRIOR FILING DATE: 2003-11-10
;  PRIOR APPLICATION NUMBER: EP 03013819
;  PRIOR FILING DATE: 2003-06-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
;   LENGTH: 726
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-872-198-120

  Query Match           99.4%;  Score 2563.5;  DB 17;  Length 726;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 89
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Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 269

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 329

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 389

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 449

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476
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RESULT 8
US-11-021-951-120
; Sequence 120, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
;  APPLICANT: HAUPTS, Ulrich
;  APPLICANT:  KOLTERMANN, Andre
;  APPLICANT:  SCHEIDIG, Andreas
;  APPLICANT:  VOTSMEIER, Christian
;  APPLICANT:  Kettling, Ulrich
;  APPLICANT:  COCO, Wayne Michael
;  TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
;  TITLE OF INVENTION:  And Diagnostic Use Thereof
;  FILE REFERENCE: 04156.0002U5
;  CURRENT APPLICATION NUMBER: US/11/021,951
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: 10/872,198
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 60/543,518
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/524,960
;  PRIOR FILING DATE: 2003-11-25
;  PRIOR APPLICATION NUMBER: EP 04003058
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: EP 03025871
;  PRIOR FILING DATE: 2003-11-11
;  PRIOR APPLICATION NUMBER: EP 03025851
;  PRIOR FILING DATE: 2003-11-10
;  PRIOR APPLICATION NUMBER: EP 03013819
;  PRIOR FILING DATE: 2003-06-18
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
;   LENGTH: 726
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-021-951-120

  Query Match           99.4%;  Score 2563.5;  DB 20;  Length 726;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         30 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 89

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 149

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        150 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 209

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 269

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 329

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 389

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 449

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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Db        450 CYTGNPLIPWDYCPISRCEGDTTPTIV 476


RESULT 9
US-08-605-221-2
; Sequence 2, Application US/08605221
; Publication No. US20030060403A1
; GENERAL INFORMATION:
;  APPLICANT:  NAKAMURA, Toshikazu
;  TITLE OF INVENTION:  THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
;  FILE REFERENCE:  2520-0101P
;  CURRENT APPLICATION NUMBER: US/08/605,221
;  CURRENT FILING DATE:  1996-03-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: HGF-A (Full length HGF)
US-08-605-221-2

  Query Match             99.4%;  Score 2563.5;  DB 8;  Length 728;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              ||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 10
US-10-813-805-10
; Sequence 10, Application US/10813805
; Publication No. US20040191902A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER  INC.
;  APPLICANT:  Hambor, John E.
;  APPLICANT:  Roach, Marsha L.
;  TITLE OF INVENTION: GROWTH AND DIFFERENTIATION OF STEM CELLS
;  FILE REFERENCE: PC25028A
;  CURRENT APPLICATION NUMBER: US/10/813,805
;  CURRENT FILING DATE:  2004-03-30
;  PRIOR APPLICATION NUMBER: US 60/459,449
;  PRIOR FILING DATE: 2003-03-31
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-813-805-10

  Query Match             99.4%;  Score 2563.5;  DB 16;  Length 728;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
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Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478
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RESULT 11
US-10-475-616-2
; Sequence 2, Application US/10475616
; Publication No. US20040236073A1
; GENERAL INFORMATION:
;  APPLICANT: Gherardi, Ermanno
;  APPLICANT:  Lietha, Daniel
;  APPLICANT:  Blundell, Thomas L
;  APPLICANT:  Chirgadze, Dimitry Y
;  TITLE OF INVENTION: The NK1 Fragment of Hepatocyte Growth Factor/Scatter
;  TITLE OF INVENTION:  Factor (HGF/SF) and Variants Thereof, and Their Use
;  FILE REFERENCE: 2502489-991180
;  CURRENT APPLICATION NUMBER: US/10/475,616
;  CURRENT FILING DATE:  2003-10-22
;  PRIOR APPLICATION NUMBER: PCT/GB02/01941
;  PRIOR FILING DATE: 2002-04-29
;  PRIOR APPLICATION NUMBER: GB 0110430.6
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-475-616-2

  Query Match             99.4%;  Score 2563.5;  DB 16;  Length 728;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 12
US-10-498-332-7
; Sequence 7, Application US/10498332
; Publication No. US20050113284A1
; GENERAL INFORMATION:
;  APPLICANT: Nakamura, Motonao
;  APPLICANT:  Higuchi, Toshio
;  APPLICANT:  Yamasaki, Yoshiki
;  APPLICANT:  Orita, Takuya
;  TITLE OF INVENTION: PHARMACEUTICAL AGENTS AND METHODS FOR
;  TITLE OF INVENTION:  TISSUE AND VASCULAR REGENERATION
;  FILE REFERENCE: 14539-016US1
;  CURRENT APPLICATION NUMBER: US/10/498,332
;  CURRENT FILING DATE:  2004-06-11
;  PRIOR APPLICATION NUMBER: PCT/JP02/13014
;  PRIOR FILING DATE: 2002-12-12
;  PRIOR APPLICATION NUMBER: JP 2002-352924
;  PRIOR FILING DATE: 2002-12-04
;  PRIOR APPLICATION NUMBER: JP 2001-380158
;  PRIOR FILING DATE: 2001-12-13
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 728
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-498-332-7

  Query Match             99.4%;  Score 2563.5;  DB 17;  Length 728;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-208;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 175
              |||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVEC 211

Qy        176 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 MTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWC 271

Qy        236 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 YTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDS 331

Qy        296 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 QYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDC 391

Qy        356 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451

Qy        416 CYTGNPLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||||||||
Db        452 CYTGNPLIPWDYCPISRCEGDTTPTIV 478


RESULT 13
US-10-133-912-18
; Sequence 18, Application US/10133912
; Publication No. US20020165358A1
;   GENERAL INFORMATION:
;        APPLICANT: Kinosaki, Masahiko
;                   Yamaguchi, Kyoji
;                   Goto, Masaaki
;                   Murakami, Akihiko
;                   Ueda, Masatsugu
;                   Higashio, Kanji
;                   Yamashita, Yasushi
;        TITLE OF INVENTION: TCF MUTANT
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Burgess, Ryan and Wayne
;             STREET: 370 Lexington Avenue, Suite 2105
;             CITY: NEW YORK
```

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;            STATE: NEW YORK
;            COUNTRY: UNITED STATES OF AMERICA
;            ZIP: 10017
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3 1/5 inch diskette
;            COMPUTER: PC'S LIMITED SYSTEM 200
;            OPERATING SYSTEM: WORD FOR WINDOWS
;            SOFTWARE: MICROSOFT WINDOWS 98
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/133,912
;            FILING DATE: 25-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/700,519
;            FILING DATE: 26-Aug-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Wayne, Milton J.
;            REGISTRATION NUMBER: 17,906
;            REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 212-683-8150
;            TELEFAX: 212-532-4285
;  INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 723
;            TYPE: AMINO ACID
;            STRANDEDNESS: SINGLE
;            TOPOLOGY: LINEAR
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-133-912-18

  Query Match             99.0%;  Score 2554;  DB 13;  Length 723;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-207;
  Matches  437;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 NTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQC 65
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37 NTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQC 96

Qy         66 LWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMI 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 LWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMI 156

Qy        126 PHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRG 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 PHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRG 216

Qy        186 LMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWE 245
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 LMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWE 276

Qy        246 YCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTP 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 YCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTP 336

Qy        306 ENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMG 365
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 ENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMG 396

Qy        366 NLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPW 425
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 NLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPW 456

Qy        426 DYCPISRCEGDTTPTIV 442
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Db        457 DYCPISRCEGDTTPTIV 473


RESULT 14
US-10-133-912-19
; Sequence 19, Application US/10133912
; Publication No. US20020165358A1
;  GENERAL INFORMATION:
;       APPLICANT: Kinosaki, Masahiko
;                  Yamaguchi, Kyoji
;                  Goto, Masaaki
;                  Murakami, Akihiko
;                  Ueda, Masatsugu
;                  Higashio, Kanji
;                  Yamashita, Yasushi
;       TITLE OF INVENTION: TCF MUTANT
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Burgess, Ryan and Wayne
;            STREET: 370 Lexington Avenue, Suite 2105
;            CITY: NEW YORK
;            STATE: NEW YORK
;            COUNTRY: UNITED STATES OF AMERICA
;            ZIP: 10017
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3 1/5 inch diskette
;            COMPUTER: PC'S LIMITED SYSTEM 200
;            OPERATING SYSTEM: WORD FOR WINDOWS
;            SOFTWARE: MICROSOFT WINDOWS 98
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/133,912
;            FILING DATE: 25-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/700,519
;            FILING DATE: 26-Aug-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Wayne, Milton J.
;            REGISTRATION NUMBER: 17,906
;            REFERENCE/DOCKET NUMBER: U-Wp-5240PCT
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 212-683-8150
;            TELEFAX: 212-532-4285
;  INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 723
;            TYPE: AMINO ACID
;            STRANDEDNESS: SINGLE
;            TOPOLOGY: LINEAR
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-133-912-19

  Query Match             99.0%;  Score 2552;  DB 13;  Length 723;
  Best Local Similarity   98.9%;  Pred. No. 1.7e-207;
  Matches  437;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALAIATAAVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              ||||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 15
US-10-149-103A-1
; Sequence 1, Application US/10149103A
; Publication No. US20040121945A1
; GENERAL INFORMATION:
;  APPLICANT: Liang, Hong
;  APPLICANT:  Sim, Kim Lee
;  APPLICANT:  Day, Clara
;  TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
;  FILE REFERENCE: 05213-0592  43170-274540
;  CURRENT APPLICATION NUMBER: US/10/149,103A
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: PCT/US00/34039
;  PRIOR FILING DATE: 2000-12-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 727
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-149-103A-1

  Query Match             98.0%;  Score 2527.5;  DB 16;  Length 727;
  Best Local Similarity   97.1%;  Pred. No. 2e-205;
  Matches  433;  Conservative    6;  Mismatches    2;  Indels    5;  Gaps    1;

Qy          2 RKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKA 61
              :|||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         33 KKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNNGLPFTCKAFVFDKA 92

Qy         62 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 RKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPW 152

Qy        122 SSMIPHEH-----SYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 176
              ||||||||     ||||||||||||||||||||||||||||||||||||||||||||||
Db        153 SSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECM 212

Qy        177 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 TCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCY 272

Qy        237 TLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQ 296
              ||||||||||||||||||:||||||:||||||||||||||| ||||||||||||||||
Db        273 TLDPHTRWEYCAIKTCADNTVNDTDVPMETTECIQGQGEGYRGTANTIWNGIPCQRWDSQ 332

Qy        297 YPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCY 356
              |||:||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        333 YPHKHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSNGQDCY 392

Qy        357 RGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWC 416
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        393 RGNGKNYMGNLSQTRSGLTCSMWNKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWC 452

Qy        417 YTGNPLIPWDYCPISRCEGDTTPTIV 442
              ||||||||||||||||||||||||||
Db        453 YTGNPLIPWDYCPISRCEGDTTPTIV 478


Search completed: October  3, 2005, 07:42:28
Job time : 239.645 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2005, 05:58:32 ; Search time 1360.31 Seconds
(without alignments)
24.255 Million cell updates/sec

Title: US-09-674-377B-2
Perfect score: 2579
Sequence: 1 ERKRRNTIHEFKKSAKTTLI.....IPWDYCPISRCEGDTTPTIV 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2576	99.9	487	4	US-09-601-040A-27	Sequence 27, Appl
2	2576	99.9	717	4	US-09-601-040A-6	Sequence 6, Appli
3	2576	99.9	717	4	US-09-601-040A-8	Sequence 8, Appli
4	2576	99.9	723	1	US-07-838-410-1	Sequence 1, Appli
5	2576	99.9	723	1	US-08-290-937B-1	Sequence 1, Appli
6	2576	99.9	723	1	US-08-290-937B-2	Sequence 2, Appli
7	2576	99.9	723	1	US-08-404-643-1	Sequence 1, Appli
8	2576	99.9	723	3	US-09-194-326-1	Sequence 1, Appli
9	2576	99.9	723	4	US-09-600-991-18	Sequence 18, Appl
10	2576	99.9	723	4	US-08-605-221-4	Sequence 4, Appli
11	2576	99.9	723	4	US-09-601-040A-10	Sequence 10, Appl
12	2576	99.9	729	4	US-09-601-040A-2	Sequence 2, Appli
13	2576	99.9	729	4	US-09-601-040A-4	Sequence 4, Appli
14	2573	99.8	723	3	US-08-030-410-3	Sequence 3, Appli
15	2570	99.7	723	1	US-08-290-937B-3	Sequence 3, Appli
16	2563.5	99.4	697	2	US-08-460-890A-50	Sequence 50, Appl
17	2563.5	99.4	697	3	US-08-167-641C-50	Sequence 50, Appl
18	2563.5	99.4	697	3	US-08-460-971A-50	Sequence 50, Appl
19	2563.5	99.4	697	3	US-08-462-040-50	Sequence 50, Appl
20	2563.5	99.4	728	1	US-07-815-333A-2	Sequence 2, Appli
21	2563.5	99.4	728	1	US-08-087-783A-22	Sequence 22, Appl
22	2563.5	99.4	728	4	US-08-605-221-2	Sequence 2, Appli
23	2554	99.0	723	3	US-09-194-326-2	Sequence 2, Appli
24	2554	99.0	723	3	US-08-700-519J-18	Sequence 18, Appl
25	2552	99.0	723	3	US-09-194-326-3	Sequence 3, Appli
26	2552	99.0	723	3	US-08-700-519J-19	Sequence 19, Appl
27	1793	69.5	574	4	US-09-600-991-2	Sequence 2, Appli
28	1460	56.6	563	4	US-09-600-991-4	Sequence 4, Appli
29	1433.5	55.6	290	4	US-08-484-841A-8	Sequence 8, Appli
30	1171	45.4	711	1	US-08-184-012C-8	Sequence 8, Appli
31	1171	45.4	711	1	US-08-334-177-2	Sequence 2, Appli
32	1171	45.4	711	2	US-08-666-082B-1	Sequence 1, Appli
33	1171	45.4	711	2	US-08-766-982-2	Sequence 2, Appli
34	1171	45.4	711	3	US-09-296-219-2	Sequence 2, Appli
35	1171	45.4	711	4	US-09-600-991-20	Sequence 20, Appl
36	1171	45.4	711	4	US-09-601-040A-12	Sequence 12, Appl
37	1171	45.4	711	4	US-09-949-016-6981	Sequence 6981, Ap
38	1171	45.4	711	5	PCT-US95-13830-2	Sequence 2, Appli
39	1114.5	43.2	716	2	US-08-766-982-1	Sequence 1, Appli
40	1114.5	43.2	716	3	US-09-296-219-1	Sequence 1, Appli
41	1054.5	40.9	790	4	US-08-991-761A-13	Sequence 13, Appl
42	1039.5	40.3	812	1	US-08-248-629A-1	Sequence 1, Appli
43	1039.5	40.3	812	1	US-08-451-932-1	Sequence 1, Appli
44	1039.5	40.3	812	1	US-08-452-260-1	Sequence 1, Appli
45	1039.5	40.3	812	1	US-08-326-785-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-601-040A-27
; Sequence 27, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; FILE REFERENCE: 0471-0161P
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-040A-27

Query Match 99.9%; Score 2576; DB 4; Length 487;
Best Local Similarity 99.8%; Pred. No. 1.1e-213;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451
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Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 2
US-09-601-040A-6
; Sequence 6, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 717
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-6

  Query Match             99.9%;  Score 2576;  DB 4;  Length 717;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
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Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 3
US-09-601-040A-8
; Sequence 8, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 717
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-8

  Query Match             99.9%;  Score 2576;  DB 4;  Length 717;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
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Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 4
US-07-838-410-1
; Sequence 1, Application US/07838410
; Patent No. 5328836
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  HIGASHIO, KANJI
;    APPLICANT:  NAGAO, MASAYA
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  TAKAOKA, HIROAKI
;    APPLICANT:  TSUDA, EISUKE
;    TITLE OF INVENTION:  PLASMIDS CONTAINING DNA ENCODING THE
;    TITLE OF INVENTION:  AMINO ACID SEQUENCE OF TCF-II, TRANSFORMED CELLS WITH THE
;    TITLE OF INVENTION:  PLASMIDS, AND PRODUCTION MEDTHOD OF BIOLOGICALLY ACTIVE
;    TITLE OF INVENTION:  SUBSTANCE USING THE TRANSFORMED CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD.
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/838,410
;      FILING DATE:  19920311
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP91/00942
;      FILING DATE:  15-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 185852-1990
;      FILING DATE:  13-JUL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WHITE, JOHN L.
;      REGISTRATION NUMBER:  17,746
;      REFERENCE/DOCKET NUMBER:  WAK 110
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Fibroblast
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  393..405
;      OTHER INFORMATION:  /note= "INTERNAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE IN ALPHA-CHAIN"
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  490..505
;      OTHER INFORMATION:  /note= "N-TERMINAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE OF BETA-CHAIN"
;    FEATURE:
;      NAME/KEY:  Domain
;      LOCATION:  605..623
;      OTHER INFORMATION:  /note= "INTERNAL AMINO ACID
;      OTHER INFORMATION:  SEQUENCE IN BETA-CHAIN"
US-07-838-410-1

  Query Match             99.9%;  Score 2576;  DB 1;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 5
US-08-290-937B-1
; Sequence 1, Application US/08290937B
; Patent No. 5648233
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, KYOJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  MURAKAMI, AKIHIKO
;    APPLICANT:  GOTO, MASAAKI
;    APPLICANT:  TSUDA, EISUKE
;    APPLICANT:  MASUNAGA, HIROAKI
;    APPLICANT:  TAKAHIRA, REIKO
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  UEDA, MASATSUGU
;    APPLICANT:  HIGASHIO, KANJI
;    TITLE OF INVENTION:  MODIFIED TCF
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,937B
;      FILING DATE:  19-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-290-937B-1

  Query Match             99.9%;  Score 2576;  DB 1;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
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Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
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Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 6
US-08-290-937B-2
; Sequence 2, Application US/08290937B
; Patent No. 5648233
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, KYOJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  MURAKAMI, AKIHIKO
;    APPLICANT:  GOTO, MASAAKI
;    APPLICANT:  TSUDA, EISUKE
;    APPLICANT:  MASUNAGA, HIROAKI
;    APPLICANT:  TAKAHIRA, REIKO
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  UEDA, MASATSUGU
;    APPLICANT:  HIGASHIO, KANJI
;    TITLE OF INVENTION:  MODIFIED TCF
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,937B
;      FILING DATE:  19-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-290-937B-2

  Query Match             99.9%;  Score 2576;  DB 1;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
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Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 7
US-08-404-643-1
; Sequence 1, Application US/08404643
; Patent No. 5658742
;  GENERAL INFORMATION:
;    APPLICANT:  HIGASHIO, KANJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  OOGAKI, FUMIKO
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, TESTA, HURWITZ &
;      ADDRESSEE:  THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/404,643
;      FILING DATE:  15-MAR-1995
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-034 (3999/35)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)-248-7000
;      TELEFAX:  (617)-248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-404-643-1

  Query Match             99.9%;  Score 2576;  DB 1;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 8
US-09-194-326-1
; Sequence 1, Application US/09194326
; Patent No. 6306827
; GENERAL INFORMATION:
;  APPLICANT: Kinosaki, Masahiko
;  APPLICANT: Ogawa, Hiromi
;  APPLICANT: Masanuga, Hiroaki
;  APPLICANT: Kobayashi, Fumie
;  APPLICANT: Yamaguchi, Kyoji
;  APPLICANT: Higashio, Kanji
;  TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
;  FILE REFERENCE: FJN-069
;  CURRENT APPLICATION NUMBER: US/09/194,326
;  CURRENT FILING DATE: 1998-11-24
;  EARLIER APPLICATION NUMBER: PCT/JP98/01221
;  EARLIER FILING DATE: 1998-03-20
;  EARLIER APPLICATION NUMBER: JP 94989
;  EARLIER FILING DATE: 1997-03-28
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: TCF-II
US-09-194-326-1

  Query Match             99.9%;  Score 2576;  DB 3;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 9
US-09-600-991-18
; Sequence 18, Application US/09600991
; Patent No. 6551991
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo
;  APPLICANT:  MICHIELI, Paolo
;  APPLICANT:  COLLESI, Chiara
;  APPLICANT:  CASELLI, Gianfranco
;  APPLICANT:  COMOGLIO, Paolo
;  TITLE OF INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP
;  FILE REFERENCE: 0471-0162P
;  CURRENT APPLICATION NUMBER: US/09/600,991
;  CURRENT FILING DATE:  2001-08-20
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-600-991-18

  Query Match             99.9%;  Score 2576;  DB 4;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211
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Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
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Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 10
US-08-605-221-4
; Sequence 4, Application US/08605221
; Patent No. 6699837
; GENERAL INFORMATION:
;  APPLICANT:  NAKAMURA, Toshikazu
;  TITLE OF INVENTION:  THERAPEUTIC AGENT FOR DISORDER IN BRAIN AND NERVE
;  FILE REFERENCE:  2520-0101P
;  CURRENT APPLICATION NUMBER: US/08/605,221
;  CURRENT FILING DATE:  1996-03-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: HGF-B (five amino acids deletion type)
US-08-605-221-4

  Query Match             99.9%;  Score 2576;  DB 4;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
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Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
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Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 11
US-09-601-040A-10
; Sequence 10, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 723
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-601-040A-10

  Query Match             99.9%;  Score 2576;  DB 4;  Length 723;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 12
US-09-601-040A-2
; Sequence 2, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
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;   LENGTH: 729
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-2

  Query Match             99.9%;  Score 2576;  DB 4;  Length 729;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
              |||||||||||||||||||||
Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 13
US-09-601-040A-4
; Sequence 4, Application US/09601040A
; Patent No. 6730657
; GENERAL INFORMATION:
;  APPLICANT: MEDICO, Enzo et al.
;  TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
;  FILE REFERENCE: 0471-0161P
;  CURRENT APPLICATION NUMBER: US/09/601,040A
;  CURRENT FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 729
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant sequence derived from Homo sapiens
US-09-601-040A-4

  Query Match             99.9%;  Score 2576;  DB 4;  Length 729;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-213;
  Matches  441;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
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Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
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Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
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Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 14
US-08-030-410-3
; Sequence 3, Application US/08030410
; Patent No. 6221359
;  GENERAL INFORMATION:
;    APPLICANT:  Komiyama, Atsushi
;    APPLICANT:  Nakahata, Tatsutoshi
;    APPLICANT:  Kubo, Tetsuo
;    APPLICANT:  Tanaka, Ryuhei
;    APPLICANT:  Kawano, Genji
;    APPLICANT:  Sudo, Tetsuo
;    APPLICANT:  Sano, Emiko
;    APPLICANT:  Kojima, Katsuaki
;    TITLE OF INVENTION:  HEMOPOIETIC STEM CELL MULTIPLIER
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Scully, Scott, Murphy & Presser
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,410
;      FILING DATE:  19930521
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8898
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 742-4343
;      TELEFAX:  (516) 742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-030-410-3

  Query Match             99.8%;  Score 2573;  DB 3;  Length 723;
  Best Local Similarity   99.5%;  Pred. No. 3.4e-213;
  Matches  440;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
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Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
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Db        212 ESYRGLMDHTESGRICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
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Db        272 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
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Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
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Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
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Db        452 PLIPWDYCPISRCEGDTTPTIV 473


RESULT 15
US-08-290-937B-3
; Sequence 3, Application US/08290937B
; Patent No. 5648233
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, KYOJI
;    APPLICANT:  SHIMA, NOBUYUKI
;    APPLICANT:  MURAKAMI, AKIHIKO
;    APPLICANT:  GOTO, MASAAKI
;    APPLICANT:  TSUDA, EISUKE
;    APPLICANT:  MASUNAGA, HIROAKI
;    APPLICANT:  TAKAHIRA, REIKO
;    APPLICANT:  OOGAKI, FUMIKO
;    APPLICANT:  UEDA, MASATSUGU
;    APPLICANT:  HIGASHIO, KANJI
;    TITLE OF INVENTION:  MODIFIED TCF
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,937B
;      FILING DATE:  19-AUG-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, PAULA A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  723 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-290-937B-3

  Query Match             99.7%;  Score 2570;  DB 1;  Length 723;
  Best Local Similarity   99.5%;  Pred. No. 6.1e-213;
  Matches  440;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ERKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 60
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Db         32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91

Qy         61 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 120
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Db         92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP 151

Qy        121 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 180
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Db        152 WSSMIPHEHSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNG 211

Qy        181 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 240
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Db        212 ESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDP 271

Qy        241 HTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 300
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Db        272 HTRWEYCAIKTCADNTMQDTDVPLETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHE 331

Qy        301 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 360
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Db        332 HDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNG 391

Qy        361 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 KNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGN 451

Qy        421 PLIPWDYCPISRCEGDTTPTIV 442
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Db        452 PLIPWDYCPISRCEGDTTPTIV 473


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